

## STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number 115431

TO: Diana Johannsen

Location: REM/2C85

Art Unit: 1634

Monday, March 01, 2004

Case Serial Number: 09692077

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

#### Search Notes

Dear Examiner Johannsen,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



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# STIC SEARCH RESULTS FEEDBACK FORM

#### Biotech-Chem Librard

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

Voluntary Results Feedback निर्माण
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
Cited as being of interest.
☐ Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Dropofforsendicompleted forms to STIC/Biotech-Chemilibrary, Remsen Bidg



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
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	AC133232 Battus no	5 241135 2		-
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	AC12301 Rattus no	0117010	119	
	AC11ESE MUS MUSCU	011050	118	
	AC126640 Rattus no	587877 D:	117	
	ACU98956 Rattus no	201/10	116	
	ACL37871 Mus muscu	111111	c 115	
	ACL39033 Mus muscu	6 227029	114	
source	AC122832 Mus muscu	226251	c 113	
FEATURES	AC098602 Rattus no	1.6 224056 10		
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	AC111454 Rattus no	1.6 223198 2		
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-	AC136825 Ratting To	11.6 81.6 220331 2	100	
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COMMENT	AC118179 Batting	41.6 81.6 218474 2		
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BULLE	ACI38325 Mus muscu	41.6 81 6 212175 2	9	
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REFERENCE	AC124563 Mus muscu	41.6 81.6 210386 1	φ.	
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ORGANISM	AC131874 Rattus no	41.6 81.6 207283	n	
SOURCE	ALS91496 Mouse TWA	41.6 81.6 206472		
KEYWORDS	AC102541 Mus muscu	41.6 81.6 205633		
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ACCESSION	AC113021 Mile muscu	41.6 81.6 199593	G	
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	AC133515 Mus muscu	41.6 81.6 185276	c	
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145	AC124534 Mis muscu	74 41.6 81.6 178449 2 AC12954		
144	AC117346 Wattus no	41.6 81.6 177675		
142	AC115905 Mus muscu	41.6 81.6 177116	o	
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ORIGIN	CDS	gene	FEATURES source		JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE	RESULT 1 HIMA2C2 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		139 ' C 141 C 142 142 143 144 C 145 C 146 C 146 C 149 C 149 C 150
/ #85 //gene="ADRA2C" //codon_start=1 //product="alpha_2-adrenergic receptor" //product="alpha_2-adrenergic receptor" //product="alpha_2-adrenergic receptor" //protein_id="ana62823.1" //protein_id="ana62823.1" //db_xref="GDB::G00-120-540" //db_xref="GDB::G00-120-540" //translation="FCTBSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCHILTVWLIAVUSLEPELIYKCDQGPGREPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIY EKBEGETPEDTGTWALLPSEWAALLPNGOQGKEGVCGASPEDEAEEEEEEEEEEEEEECEP OAVPVSBASACSPPLQOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFT PVLAVVIGVFVLCWFPFFF"	/gene="ADRA2C"	/organism="Homo sapiens" /mol_type="genomic_DNA" /db_xref="taxon:9606" /map="4p16.3-p15" /clone="pCRA2" /cell_line="neuroblastoma SK-N-SH" /tissue_type="neuroblastoma" /dev_stage="adult" 1.885	Taipei, Taiwan, 11221 ROC. Location/Qualifiers 1885	Bou bmi ang	817-823 (1990)	yvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. also 1 to 885)  A.C., Ho.T.F. and Chang, N.C.  tro amplification by polymerase chain reaction of a parrencoding the third by polymerase.	HUMA2C2 Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds. M38742.1 GI:177867 Alpha-2 adrenergic receptor. Homo sapiens	ALIGNMENTS	41.6 81.6 241629 2 AC097388 AC097388 Rattus no 41.6 81.6 241726 2 AC097121 AC097121 AC097121 AC097121 Rattus no 41.6 81.6 241891 2 AC132675 AC132675 AC132675 Rattus no 41.6 81.6 244366 2 AC115313 AC0950 AC120850 Mus muscu 41.6 81.6 244388 2 AC120850 AC132065 Rattus no 41.6 81.6 244455 2 AC121672 AC132065 Rattus no 41.6 81.6 247180 2 AC132065 AC132065 Rattus no 41.6 81.6 247180 2 AC10863 AC10863 Rattus no 41.6 81.6 247504 2 AC111320 AC11320 Rattus no 41.6 81.6 247504 2 AC111320 AC11320 Rattus no 41.6 81.6 247505 2 AC135327 AC11320 Rattus no 41.6 81.6 247505 2 AC135327 AC11320 Rattus no AC135438 Rattus no

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AUTHORS
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Zabarovsky,E.R.
Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (16-MAY-1001) Microbiology
                                                       Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
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AX350489.1 GI:18616091
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Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kyasha,S.M., Podowski,R.M., Muravenko,O.V., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitaky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Pred. No. 0.0017;
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Catarrhini; Hominidae;
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Sequence
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Expansion of the alpha 2-adrehergic receptor subtype, characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
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Au-Young, J. and Seilhamer, J. J.
Composition for the detection of signaling
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
                                                                                                                            Original source text: Human placenta Draft entry and computer-readable sec by J.W.Lomasney, 03-WAY-1990, for rel
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                alpha-2-adrenergic receptor; plasma membrane receptor-coupled G protein.
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/gene="ADRA2B"
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                                           /map="2"
                                                                                                               Location/Qualifiers
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Query Match
100.0%; Score 51; DB 6; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GDB:GOO-120-539"
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VLATLRGQVLLGRGVUAAIGGOWWRRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSVS
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LGAICPKHCKVPHGLFQPFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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/note="alpha-2-adrenergic receptor (alpha-2
/name 'ADRA2RL1'"
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( Mus musculus

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Mammalia; Eutheria; Rodentia; St

1 (bases 1 to 133405)
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Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                     sequence.
AL662790
AL662790.21
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Mouse DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.
Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
CHU Ranqueil, Toulouse 31403, France
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Cayla, C., Schaak, S., Bouloumie, A., Devedjian, J.C. and Paris, H.
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Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.,
Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.
Alpha2C2-adrenergic receptor gene
Unpublished
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Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_starte_1
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RQPRDHGGALASAILFALASVASAREVNGHSKSTCSKEEGETPEDTGTRALFPSWAA
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LGAICPKHCKVPHGLFQFFWIGYCNSSLMPVIYTIFNQDFRRAFRRILCRPWTCTAW
                                                                                                                                                                                                                                                            133405 bp DNA
sequence from clone RP23-53E2 on
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/gene="alpha2C2AR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="brain fetal genomic library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Organism="Homo sapiens"
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(db_xref="taxon:9606"
(chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 9;
Pred. No. 0.0015;
Mismatches 0
                                                                                                            Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9944;
                                                                                                                                                                                                                                                        chromosome
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                                                                                                    Euteleostomi;
; Murinae; Mus.
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me 11, complete
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SOURCE ORGANISM VERSION KEYWORDS

Homo sapiens (human) Homo sapiens

ACCESSION DEFINITION

AF005900.2

GI:33439705

Homo sapiens alpha2B-adrenergic complete cds.
AF005900

AF005900

RESULT 7 AF005900

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088

ORIGIN

FEATURES

Bource

Location/Qualifiers

JOURNAL

antigenic peptides Patent: WO 0206108

REFERENCE AUTHORS TITLE

VERSION KEYWORDS

ACCESSION

AX548756 Sequence 41 from Patent AX548756 AX548756.1 GI:25813686

SOURCE

ORGANISM

Homo sapiens (human)

RESULT 6 AX548756 LOCUS

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ORIGIN

Chromosome 2.

Query Match Best Local Similarity Matches 51; Conserv

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                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, Swisspard; Tr., TREMBL; We, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9337
Birren,B., Linton,L., Nusbaum,C., Lander,B., Abraham,H., Allen,N Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D. Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus chromosome 11 clone RP23-53E2 map 11, SEQUENCE, 6 unordered pieces.
AC069060
AC069060.4 GI:29029385
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAAGAGTG 50
                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Rodentia, 1 (bases 1 to 216444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-53E2 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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Center code: SC
Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                               Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                       Unpublished
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Pred. No. 0.091;
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Sciurognathi; Muridae;
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JOURNAL
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CE 3 (bases 1 to 216444)

RES Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
MacCionald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
MacCionald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Howland, J.C., Iliev.I., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McSwan, P., McGurk, A., McKernan, K., McPheeters, R., McIdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T., Miranda, C., Pierre, N., O'Neil, D., Oliver, T., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vest, M., Viel, R., Vo, A., Wisson, B., Wi, X., Wyman, D., Ye, W.J., Volan, T., Tarwers, M., Trigilio, J., Vo, A., Wisson, B., Wi, X., Wyman, D., Ye, W.J., Volan, T., Tarwers, M., Trigilio, J., Vo, A., Wisson, B., Wi, X., Wyman, D., Ye, W.J., Volan, T., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Talamas, J., Tarwers, M., Talamas, T., Tarwers, M., Talamas, T., Tarwers, M., Talamas, T., Tarwers, M., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 18, 2003 this sequence version replaced gi:15291107. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                             Center clone name: 53 B 2

------ Summary Statistics
Sequencing vector: M13; M77815; 25% of reads
Sequencing vector: Plasmid; n/a; 75% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 215352 bases at least Q40
Consensus quality: 215357 bases at least Q30
Consensus quality: 215951 bases at least Q20
Insert size: 215944; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center code: WIBR
Quality coverage: 12.0 in Q20 bases; sum-of-contigs
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<sup>\*</sup> NOTE: This is a 'working draft' sequence. It currently

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 6 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1 12827: contig of 12827 bp in length

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REFERENCE
AUTHORS
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KEYWORDS
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ASP427259
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 92.0
       calibrations
J. Mol. Evol
               Douzery, E.J.P., Delauc, F., Stanhope, M.J. and Huchon, D. Local molecular clocks in three nuclear genes: divergence times for rodents and other mammals, and incompatibility among fossil
                                                                                                     Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J., Catzeflis,F., de Jong,W.W. and Douzery,E.J.
Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear genes Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                           Anomalurus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Anomaluridae;
                                                                                                                                                                                                                                                                  A2AB gene; alpha 2B
Anomalurus sp.
                                                                                                                                                                                                                                                                          AJ427259.1 GI:21655549
A2AB gene; alpha 2B adrenergic receptor.
                                                                                               2082125
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clone_end:T7
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|38991. .216444
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40797. .138890
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16784. .25277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment
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16683: contig of 3756 bp in length
16783: gap of 100 bp
25277: contig of 8494 bp in length
25377: gap of 100 bp
40796: contig of 15319 bp in length
40796: gap of 100 bp
138890: contig of 98094 bp in length
13890: gap of 100 bp
216444: contig of 77454 bp in length
(2003) In press
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lone_lib="RPCI-23 Female Mouse
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92.0%;
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Pred. No. 0.088;
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OCAAR2B
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                                 Madsen, O.
Direct Su
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               Submitted
                                                                                                    Direct Submission
Submitted (16-DEC-1997) O. Madsen,
Department of Biochemistry, PO Box
                                                                                                                                                                                                    Stanhope, M.J., Madsen, O., Waddell, V.G., and Springer, M.S.
Highly congruent molecular support for a of edemic African mammals
                                                                                                                                                                                                                                                                       alpha adrenergic receptor; subtype 2B.
Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                             Madsen, O.
                                                            Revised by [3]
3 (bases 1 to 1183)
                                                                                             NETHERLANDS
                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus gene encoding alpha
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                                                                                                                                                                                                                                                                                                                                                                                                          subtype 2B, partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                               OCAAR2B
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Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences d'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 1185)
Douzery, E.J.P.
          Submission
ted (15-NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene='A2AB"
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RALENNSKATPRRIKRIILIVWLIAAVISLPPLIYKCDGGPQPRGRPQCKLNQEAWYI
RALENNSKATPRRIKRIILIVLARISLYVLARSURRGPRINGRPGQGESKQTPPVPGGAPAS
CGASAEEEAEEEEEEEEEEEEEEEEEEEEDGATPUSDPGARALFSSWALLPNSGGQYKGA
HVGTNGGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQCKCPH
CT-m"
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/gene="A2AB"
/number=1
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97.8%;
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Pred. No. 0.14;
0; Mismatches 1;
 O. Madsen, University
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                                                                                             University of Nijmegen,
9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                           for a diverse superordinal clade
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of Nijmegen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Highly congruent molecular support for a diverse superordinal clade of edemic African mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Springer, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanhope, M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha adrenergic receptor.
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On Nov 17, 1999 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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SGASLEEEAEEEEEEEEEEEEEPQAVPVSPASVGSPPLQQPQGSRVLATLRGQVLVGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGAMSGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
                                                                                                                                                                       codon_start=2/
                                                                                                                                                                                                           db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                             location/Qualifiers
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|mol_type="genomic DNA"
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gene encoding alpha
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Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                      PO Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PO Box 9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                   Madsen, University of Nijmegen,
Box 9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Good, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacConnald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mardonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mardonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mardonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Minoya, T., Mihoya, T., Naylor, J., Nguyen, C., Micol, R., Norbu, C., McEwan, P., McKernan, K., Melderim, J., Meneus, L., Mihoya, T., Norbu, C., McEwan, P., McKernan, K., Melderim, J., Meneus, L., Mihoya, T., Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Reserti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Sewary, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Trajanan, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Zhimmer, A. and Zody, M.

Direct Submission
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                                                                                                                                                                                                                                                                                 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavki, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Carerira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Kells, C., Landers, T., Levine, R., Landers, T., Landers, T., Levine, R., Landers, T., Levine, R., Landers, T., Levine, R., Landers, T., Landers, T., Levine, R., Landers, T., Landers, Landers, Landers, Landers, Landers, Landers, Landers, Landers, Land
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Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Malor, J., Murphy, T., Naylor, J., Nguen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research, 320 Charles Street, Cambridge, 3 (bases 1 to 206933)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus clone RP23-59D8,
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Birren,B., Nusbaum,C.
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AKLPTLATPVASASEANGPSKPAGEKEBGETPEDPGTQALPEGHATTLNSGQGPGEGV
SGASLEEAEEEEEEEEDEPGAVPVSPASVGSPLQQPGSRVLATLRGQVLVFGV
VGAMSGXWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
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* consists of 10 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
provided by the submittor.
* This sequence will be replaced
by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 30761 30860: gap of 100 bp
* 30861 31511: contig of 651 bp in length
* 31511 contig of 655 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: phrap; version 0.960731 Consensus quality: 204894 bases at least Q40 Consensus quality: 205493 bases at least Q40 Consensus quality: 205493 bases at least Q20 Insert size: 205000; agarose-fp Insert size: 205003; sum-of-contigs
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Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                       /note="assembly_fragment"
31612. .36489
                                                                                                                                                         vector_side:left"
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                                                                                                                                                                                                                                                             /clone="RP23-59D8"
/clone_lib="RPCI-23 Female Mouse
                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3649: contig of 4878 bp in length
37765: contig of 4176 bp in length
77865: gap of 100 bp
77865: gap of 100 bp
91260: contig of 13395 bp in length
91360: gap of 100 bp
111714: contig of 20354 bp in length
111814: gap of 100 bp
134504: contig of 22690 bp in length
134504: gap of 100 bp
165128: contig of 30524 bp in length
165228: gap of 100 bp
167681: contig of 30524 bp in length
197681: contig of 30524 bp in length
197681: gap of 100 bp
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SOURCE
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AC103291
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Best Local
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                                           Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Foster, M., Fernandez, S., Pinley, M., Flagg, N., Forbes, L., Foster, M., Foster, M., Gebisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Hernandez, S., Hines, S., Hadinn, S.L., Hodgson, A., Hogues, M., Hernandez, R., Hadins, S.L., Hodgson, A., Hogues, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D.Marie.,
Allen, C., Allen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC103291 215065 bp DNA linear HTG 09-N
Rattus norvegicus clone CH230-13104, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 215065)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anquiano, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "ector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
165229, 197581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note≈"assembly_fragment'
)1361. .111714
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36590. .77765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%;
93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .91260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43.2; DB
Pred. No. 0.11;
0; Mismatches
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Montemayor, J., Moore, S., dasa, M., Murphy, M., Nair, L.,
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FEATURES

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Nwaotekamah, O., Okwaomu, G., Olarspunsaspon, A., Pal, S., Parks, K., Pateterak, S., Paul, H., Parez, A., Perez, L., Pernancoh, C., Plapper, F., Polindexter, A., Popovic, D., Primas, E., Pul, L. L., Pauzo, M., Olitoz, J., Racilin, E., Revers, K., Regisr, M.A., Reigh, R., Ratilly, B., Ratill
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REFERENCE AUTHORS TITLE

TITLE JOURNAL

JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
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AC112440
                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cheveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Braper,H., Egeotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Foorbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC112440 222507 bp DNA lin
Rattus norvegicus clone CH230-144K15, WORKING
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                                                                                                                                                                                                                                                                                                                                                          Rattus.
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Similarity 93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_end_extension clone_end:Sp6" 213358. .215065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_end_extension
clone_end:Sp6"
211345. 212647
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clone_end:T7"
2440._.3271
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202478. .203219
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:lone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="CH230-13104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
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_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.2; DB Pred. No. 0.11;
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DRAFT SEQUENCE, 4
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data.html).

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AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One On Nov 15, 2002 this sequence version replaced gi:22856702.

The sequence in this sequence version replaced gi:22856702.

and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas individual sequence contigs are ordered and oriented, and separated may extend beyond the ends of the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladdin, S.L., Hodgson, A., Hogues, M., Jackson, A., Jackson, J., Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                         Center project name: GRYP

Center clone name: CH230-144K15

Center clone name: CH230-144K15

Assembly program: Phrap; version 0.990329

Consensus quality: 206532 bases at least Q40

Consensus quality: 208648 bases at least Q30

Consensus quality: 209801 bases at least Q20
                                                                                                                                                                                                                                                                                                                      Center code: BCM Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
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Best Local Similarity
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RS Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Ballen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Ballen, H., Barastead, M., Barastead, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bahay, C., Burch, P., Burrell, K., Calderon, E., Chacher, K., Carteer, K., Cavacos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Draper, H., Dugan-Rocha, S., Duramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Bscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus (Norway zat)
Eukarvor- Gicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC126653.4 GI:30581479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 226214)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53078
53178
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57499 ..58533
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109071. .110316
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62821. .64890
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|mol_type="genomic DNA"
|db_xref="Laxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="CH230-144K15"
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1e CH230-236K3, WORKING DRAFT SEQUENCE,
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Gaps

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HTG 13-MAY-2003

Length 222507; Indels

REFERENCE AUTHORS TITLE

JOURNAL,

REFERENCE AUTHORS TITLE

Worley, K.C.

Unpublished

JOURNAL,

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Praser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerara, W., Gueraratte, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hlyk, S., Hamilton, E., Hogues, M., Hollins, B., Howells, S., Hlyk, S., Khan, Z., King, L., Kowas, C., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kaeft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longare, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lewis, L., Li, Z., Liu, J., Mahneshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Martin, K., Martin, K., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mangum, B., Mapua, P., Martin, K., Martin, K., Martinez, E., Mangum, S., Muries, S., Munidasa, M., Murphy, M., Nair, J., Newton, N., Muyern, N., Norris, S., Monsen, E., Pull, L.-L., Plapper, F., Poindextex, A., Popovic, D., Primus, E., Pull, L.-L., Plapper, F., Poindextex, A., Popovic, D., Primus, E., Pull, L.-L., Phaze, C., Rockey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Stetmle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trabor, P., Taylor, C., Taylor, T., Thomas, S., Tingey, A., Trabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Jaylor, C., Wallsana, S., Tingey, A., Trabor, P., Taylor, C., Taylor, T., Thomas, N., Jaylor, C., Wallon, R., Weins, C., Marcen, R., Weins, K., Morte, F., Williasana, D., Wallon, L., Walker, B., Wang, J., Wallon, R., Weins, R., Santh, D., Kein, H., Worley, K., Wilte, F., Williasana, D., Wallon, L., Woolen, H., Worley, K., Wilte, F., Song, J., Zhou, X., Zhou, X., Zhou, S., Dunn, D., von, V., Wallon, R., Smith, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13.-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:22857176.
The sequence in this seguence version replaced using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold spandividual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 226214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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Center project name: GKJW
Center clone name: CH230-236K3
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 201903 bases at least
                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                             Project Information
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

REFERENCE TITLE JOURNAL

AUTHORS

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SOURCE
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyal-bechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Bgan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Rattus norvegicus clone CH230-21B17,
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 287497)
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1975. .3636
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224751. .226214
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221697. .223335
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3737. .4954
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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93.8%;
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AL Submitted (23.NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

The sequence in this sequence version replaced gi:23321740.

and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.cmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated contidual sequence contigs are ordered and oriented, and separated contigs within a contig-scaffold that consist entirely of whole shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Best Local (
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AC095903.9 GI:24940776
                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGAG 48
                                                                           Rattus norvegicus clone CH230-10L19,
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                                                                                                                            AC095903
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                                                   5 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This sequence may represent more than one clone.

NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently is not known and their order in this sequence record is
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281734
283732
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276816
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280003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_contig"
271588. .273871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256804.
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254752. 255877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="wgs_contig"
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258325. .259516
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101862. .103060
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97147: gap of unknown length
101761: contig of 4614 bp in length
101861: gap of unknown length
254651: contig of 152790 bp in length
254751: gap of unknown length
25824: contig of 373 bp in length
271487: contig of 3133 bp in length
271487: contig of 3133 bp in length
271587: gap of unknown length
276515: contig of 1163 bp in length
276515: gap of unknown length
276815: gap of unknown length
276812: contig of 1397 bp in length
3280102: gap of unknown length
3280102: gap of unknown length
3281633: contig of 1531 bp in length
281633: gap of unknown length
281831: gap of unknown length
281831: gap of unknown length
283731: contig of 1939 bp in length
283831: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                        84.78;
93.88;
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.258224
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                                                                                                                                                                                                                                                                                                                                                Score 43.2; DB 2;
Pred. No. 0.11;
0; Mismatches 3,
                                                               DNA linear
9, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                 Length 287497;
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                                                         HTG 13-NOV-2002
IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                 Gaps
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REFERENCE AUTHORS

TITLE JOURNAL

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (14-JAN-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA

COMMENT

Center:

----- Genome Center er: Baylor College of Medicine

Assembly program: Phrap; versior Consensus quality: 256550 bases

r clone name: בייביר בירי--- Summary Statistics בירי הוסקרמה: Phrap; version 0.990329

least Q40

TITLE
JOURNAL
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AUTHORS
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JOURNAL

Worley, K.C. Direct Submission Unpublished 2 (bases 1 to 287497)

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Checland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hernandez, R., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Sohnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.
                                              Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On NOV 13, 2002 this sequence version replaced gi:22772685. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-SEP-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 293183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhauseern,A., Weise,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
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                                                                                                                                                                                                                                                                                                                                                                 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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                                                                                                                                                                                                                                                                                                             Direct Submission
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Nov 13, 2002 this sequence version replaced gi:22772685.
e sequence in this assembly is a combination of BAC based reads
d whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 293183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 293183)
                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center, Department of Medicine, One
                                                                                                                                                                                                          ORIGIN
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                                    Query Match
Best Local Similarity
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contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                          (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas as scaffold, within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
table.
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   runs of N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48443
289478
289578
291427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44342
44442
48343
                                                                                                                                                                                                                                                                           9810. .10659
/note="clone_boundary
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/note="wgs_end_extension
clone_end:Sp6"
                                     end_sequence:BH307132"
231098. .232521
                                                                                          clone_end:Sp6
                                                                                                                 /note="wgs_contig"
181343. .182203
/note="clone_boundary
                                                                                                                                                                          /note="wgs_contig"
48443. .51434
                                                                                                                                                                                                                                                                                                                                     /clone="CH230-10L19"
                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44441: gap of unknown length
48342: contig of 3901 bp in length
48442: gap of unknown length
289477: contig of 241035 bp in length
289577: gap of unknown length
291426: contig of 1849 bp in length
291526: gap of unknown length
293183: contig of 1657 bp in length.
                                                                                                                                                                                                                                    sequence:BH307090"
                                                                                                                                                                                                                                                                                                                                                                                type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44341: contig of 44341 bp in length
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Conservative

0

Score 43.2; DB Pred. No. 0.11; 0; Mismatches

BB 2 u -

Length 293183; Indels

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Gaps

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93.8%;

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46; Conservative
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AJ427260.1 GJ:21665824

AJ427260.1 GJ:21665824

A2AB gene, alpha 2B adrenergic receptor.

Castor canadensis (American beaver)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.

Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences c'Evolution, Lab. Paleonco., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Douzery, E.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Evol. (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Douzery, E.J.P., Delsuc, F., Stanhope, M.J. and Huchon, D. Local molecular clocks in three nuclear genes: diverge rodents and other mammals, and incompatibility among f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
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/gene="A2AB"
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="alpha 2B adrenergic receptor"
/prottein_id="CAD20298.1"
/db_xref="GI:21665885"
/db_xref="GO:20166585"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="A2AB"
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                                                                                                                                                            84.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _type="genomic
                                                                                                                                 0;
                                                                                                                     Score 43; DB 10; Length 1191;
Pred. No. 0.17;
0; Mismatches 5; Indels
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gene for alpha 2B adrenergic
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                                                                                                                                      RS Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N., Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N., Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N., Birren, B., Musbaum, C., Lander, R., Bastien, V., Bloom, T., Charg, J., Chang, J., Choepel, Y., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Dode, S., Dode, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Pitzderald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Hall, J., Hotton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Madori, J., Manning, J., Mathews, C., McClarthy, M., Madidin, M., Mabbitt, R., MacLean, C., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Roman, J., Schupback, R., Gamera, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Falamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wyman, D., Young, G., Zaihoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Birren, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyd, S., Goyette, M., Graham, L., Grand-Pierre, N., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mensey, C., Miroya, T., Mlenga, V., Murphy, T., Naylor, J., Myuyen, C., Nicol, R., O'Connor, T., O'Donnell, P., O'Neil, D., Raymond, C., Retta, R., Rieback, M., Riley, R., Kiese, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wman, D., Vessiltev, H., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Ye, W.J., Young, G., Jones, L., Zimmer, A., and Zody, M., Ye, W.J., Young, G., Jones, J., Charles, J., Teefaye, S., Theodore, J., Johnson, S., Schauer, J., Zembek, L., Zimmer, A., and Zody, M., Ye, W.J., Young, G., Jones, J., Lander, J., Johnson, J., Zembek, L., Zimmer, A., and Zody, M., Ye, W.J., Young, G., Jones, J., Lander, J., Johnson, J., Zembek, L., Zimmer, A., and Zody, M.
            Submitted (22-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 22, 2003 this sequence version replaced gi:28412068. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 217323)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 217323)
Birren,B., Nusbaum,C. and Land
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Mus musculus (house mouse)
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Mus musculus clone RP23-20118, WORKING
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118766
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                                                                                                                                          Conservative
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118766. | 12000
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                                                                                                                                                                                                                                                          vector_side:right"
                                                                                                                                                                                                                                                                                                                                       210473.
                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
131658. .210372
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
123638. .131557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-20L18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment"
120960. .123537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-23 Female Mouse BAC"
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118765: gap of 100 bp
120859: contig of 2094 bp in length
120959: gap of 100 bp
123537: contig of 2578 bp in length
123637: gap of 100 bp
131557: contig of 7920 bp in length
131657: gap of 100 bp
210372: contig of 78715 bp in length
210472: gap of 100 bp
210373: contig of 6851 bp in length
                                                                                                                                                              83.5%;
91.8%;
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                                                                                                                                          0;
                                                                                                                                                                 Score 42.6; DE
Pred. No. 0.16;
                                                                                                                                          Mismatches
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                                                                                                                                        4.
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AUTHORS
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                                                                                                                                                                                                                          CE 3 (bases to 232202)

RS Birren, B., Nusbaum, C., Lander, E., Nobelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cammarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., MacCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., MacLean, C., Noguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasemy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tayerers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Chappe, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                  Direct Submission
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Center: Whitehead
Center code: WIBR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                            HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN Mus musculus (house mouse)
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5 unordered pieces.
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e 3 clone RP23-476G18 map 3,
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Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Garham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Limblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., McCarthy, C., Nardan, C., Nardhy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Norbu, C., Norman, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Suvramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Tavisi, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

AL Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome R. 10 of the Control of the Cartes, Cambridge, MA 02141, USA 2 (bases 1 to 232202)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Colling,S., Collymore,A., and Lander,E. me 3, clone RP23-476G18

On Dec 15, 2003 this sequence version replaced gi:28927750 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Submitted (15-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Institute/ MIT Center for Genome Research

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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute center code: SC
Web site: http://www.sanger.ac.uk
                                                                                              Submitted (02-UIL-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirles:
On Jul 2, 2003 this sequence requests: clonerequest@sanger.ac.uk Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence from the whole genome shotgun alone has only been used where it has phred quality of at least 30.
During sequence assembly data is compared from overlapping clones.
                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                     Chapman,
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                            BX465209.7 GI:32439584
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse DNA sequence from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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143697
148480
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Center project Information
Center project name: 122818
Center clone name: 476_G_18
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72078
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/clone_lib="RPCI-23 Female Mouse BAC"
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/mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
chromosome="3"
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143596: contig of 71519 bp in length
143696: gap of 100 bp
148479: contig of 4783 bp in length
148479: contig of 4783 bp in length
200240: contig of 51661 bp in length
1232022: contig of 51862 bp in length
1232022: contig of 51862 bp in length
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91.8%;
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m clone RP23-359C20 on chromosome X,
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AUTHORS
TITLE:
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AL672046/c
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Matches

FEATURES

RESULT 22

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

KEYWORDS SOURCE VERSION ACCESSION DEFINITION BX465209/c

ORGANISM

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AL Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

On May 16, 2002 this sequence version replaced gi:2039178.

Where difference assembly data is compared from overlapping clones. together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with regions were either double-stranded or sequence submission. This sequence was finished as follows unless otherwise noted: all chemistry or covered by high quality data (i.e., phred quality sequences and trepeats; all regions were covered by high quality data (i.e., phred quality sequences and repeats; all regions were covered by at least assembly was confirmed by restriction of men all subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Where differences are found these are annotated as variations variation anotation may not be found in the sequence submission corresponding to the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by high quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the occasion of the clone being a yAC.

The following abbreviations are used to associate primary accession on the wormer database can be found at high compression of the clone being a yAC.

THE SMBL; Sw; SWISSPROT; Tr: TREMBL; Wp:, WORMPEP database can be found at the reproper accust, Projects/C-elegans/wormpep RP23-359C20 is constructed by the group of Poieter de Jong.

VECTOR: pBACe3.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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/mol type≈"genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186272 bp DNA linear ROD 22-MAY-2002
on clone RP23-299F14 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.2; DB 10;
Pred. No. 0.23;
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FEATURES

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REFERENCE
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AC128836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Barca, E., Baden, H., Benahmed, F., Baldwin, D., Bandaranaike, D., Burrell, K., Calderon, B., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Catter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Cokreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, C., Davy, Carroll, L., De Dederich, D., Davila, M., Davis, C., Davila, A., Ganda, C., Dunh, H., Divya, K., Degen, C., Davila, A., Garner, T., Garza, M., Gebraer, C., Eigel, R., Garcia, A., Garner, T., Garza, M., Gebraegoorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Gevara, W., Ghorandez, S., Hinden, S., Handlor, C., Hamilton, C., Hamilton, K., Hernandez, J., Hernandez, J., Hewel, A., Henderson, N., Hernandez, J., Hernandez, J., Hodgson, A., Hogues, M., Jackson, A., Jackson, A., Jockson, A., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Moreis, E., Mollos, M., Morris, S., Mollos, M., Morris, S., Mollos, M., Morris, S., Montemayor, J., Moore, S., Mollos, M., Morris, S., Mollo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus clone CH230-485K2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, Sw., SWISSPROT, Tr., TREMBL, Mp., WORMPEP, Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC128836.3 GI:25139497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-299F14 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATGAAGAGGAAGAGGAAGAGAGAGGAGGAGGAAGAG 185040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 189624)
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/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-299F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="RPCI-23"
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93.6%;
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Pred. No. 0.2;
0; Mismatches
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KEYWORDS VERSION ACCESSION 밁

Snoo

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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:22855866.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Revter, M., Richarde, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z, Sorelle, R., Sosa, J., Sneed, A., Trong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walder, B., Wang, J., Warren, J., Walder, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Warren, R., Wei, X., Taylor, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Genome Sequencing Consortium.
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3 (bases 1 to 189624)
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    Genome Center
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

REFERENCE AUTHORS

JOURNAL TITLE

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NOTE: Estimated insert size may differ from sequence length
(see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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8263: contig of 8263 bp in length 8363: gap of unknown length
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AUTHORS
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KEYWORDS
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Names 1 to 189869

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Marie, M., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Alder, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brant, N., Buhay, C., Burch, P., Burchl, F., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Ch
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC128202.3 GI:25139218
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGA 47
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35358. .37673
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/mol_type="genomic_DNA"
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112776: contig of 77419 bp in length
112876: gap of unknown length
112876: gap of unknown length
168816: contig of 53940 bp in length
166916: gap of unknown length
166916: gap of unknown length
166916: gap of unknown length
169095: gap of unknown length
171730: contig of 2079 bp in length
171730: contig of 2635 bp in length
171830: gap of unknown length
171830: gap of unknown length
188624: contig of 17794 bp in length.
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Pred. No. 0.2;
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the 3 (bases 1 to 18988)

RS Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (20-NOY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23908157.

The sequence in this assembly is a combination of BAC based reads (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwonu, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Ouiroz, J., Rachlin, E., Reeves, K., Regier, M., Riggs, F., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, R., Ruis, S.J., Sanderes, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Watren, R., Wei, X., White, F., Wang, G., Wilson, R., Wilson, R., Wei, X., White, F., Wanght, D., Waish, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinstock, G. and Gibbs, R.A. Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 189886)
Worley, K.C.
Direct Submission
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GZMW
Center clone name: CH230-423919
Assembly program: Phrap; version 0.990329
Consensus quality: 175673 bases at least Q40
Consensus quality: 175673 bases at least Q30
Consensus quality: 17988 bases at least Q30
Consensus quality: 17900 bases at least Q30
Consensus quality: 17904 bases at least Q30
Consensus quality: 17946; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 2 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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REFERENCE
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TITLE
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VERSION
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Best Local Similarity
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                            AL691481
AL691481.15 GI:22213670
HTG; Atp5h; CpG island; Eno3.
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Al691481

Al691481

Mouse DNA sequence from clone RP23-173C3 on chromosome 4 Contains a muscle enclase 3 beta (Enc3) pseudogene, a mitochondrial H+transporting ATP synthase F0 complex subunit d (Atp5h) pseudogene
                                                                                Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 230127)
                                               During sequence assembly data is compared from overlapping clones
                                                                                                                    Center code: UK-MRC
                                                                                                                                                                                                             Submitted (17-MAR-2003) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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/note="clone_boundary
clone_end:Sp6
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clone_end:Sp6"
187014. 188573
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clone_end:Sp6"
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clone_end:T7"
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'clone="CH230-423P19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.7%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence: BZ183966"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence: BZ183964"
                                                                                                                                                                                                                                                                                                                                                                                               complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.2;
Pred. No. 0.
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replaced gi:21748253.
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality -= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the entire insert of clone RP23-173C3 The true left end of clone RP23-426J14 is at 226462 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence day from the whole genome shotgun alone has only been used where it his a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
the clone being a YAC.
RP23-173C3 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VECTOR: pBACe3.
                                                                                                                                                                                                                       /note="5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1268. 1295
/note="28.0 copies 1 mer T 20% conserved"
complement (1344. .2435)
/note="L1 repeat: matches 3932. .5048 of consensus"
complement (2570. .2768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1258. .1284
/note="3.0 c
1260. .1275
                                                                                         /note="3.0 copies 5 mer complement (5128. .5791)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="26.0 copies 2 mer TG 86% conserved"
complement(956. .1118)
/note="B3A repeat: matches 8. .178 of consensus"
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/note="2.5 <
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/db_xref="taxon:10090"
/chromosome="4"
                                                        note="L2 repeat: matches 2228. .2955 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ll repeat: matches 4623. .4828 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="4.0 copies 4 mer TTTC 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="4.5 copies 4 mer TTTA 29% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: GSS: Em:AZ561521"
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695
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                                                                                                                                                                                                                                                                                                                .9 copies 12
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copies 7 mer ATCATTC 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                              copies 6 mer TTTGAT 21% conserved
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ଜ
                                                                                                                       AGTGA 21% conserved"
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/note="LX9 repeat: matches 6857. .7165 of consensus"
                                                                                       /note="9.0 copies 2 mer CT 36% conserved" complement (13947. .14255)
                                                                                                                                                                                                                                                                                                      complement (13548. .13856)
/note="Lx9 repeat: matches 7125. .7451 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                      /note="2.2 copies 5 mer TATTT 22% conserved"
complement(13323. .13477)
/note="Lx9 repeat: matches 7477. .7644 of consensus"
                                                                                                                                                                                                                       /note="16.3
13907. .1392
                                                                                                                                                                                                                                                                      13860.
                                                                                                                                                                                                                                                                                                                                       /note="25.5 copies 2 mer AC 93% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13292. .j
/note≃"2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (12315. .13123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note≈"Lx repeat: matches 5801.
12565. .13254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="2.0 copies 21 mer TGGTTAAAAATTGAAACTATT 59%
conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match: GSS: Em:AZ334877"
3292. .13302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="13.2 copies 5 mer AAAAG 57% conserved"
11943. .11965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="23.0 copies 1 mer A 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
11875. .11888
/note="2.3 copies 6 mer Aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     match: proteins: Sw:P25704 Sw:P15429 Tr:BAB22137 Tr:AAH13460 Sw:P13929 Sw:P21550 Sw:P51913 Tr:AAH24644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (10509. .11722)
/gene="bM173C3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="bM173C3.1 (enolase 3, beta muscle (Eno3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10489. 10500 TO CONSEN

/note="2.0 copies 6 mer CAGGGA 24% conserved"

complement (10509. 11722)

/gene="bM173C3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="3.7 copies 3 mer AAC 22% conserved" complement(9891 . .10099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 15. .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORRIA2 repeat; matches 1. .327 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9973. .9013
| note="20.5 copies 2 mer TG 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8845. .8883)
/note="WIR repeat: matches 58. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="2.5 copies 4 mer ATCT 20% conserved" complement (8845. .8883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pote="48.5 copies 2 mer TC 52% conserved"

7510. 7519

Pote="2.0 copies 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="2.0 copies 9 mer ATCATTATT 36% conserved"
7046: .7063
/note="4.5 copies 4 mer TTTA 27% conserved"
                                                                                                                                                                                                                  .13925
                                                                                                                                                                                                                                                                11.2 copies 6 mer CTTCTC 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .12233
                                                                                                                                                              .3 copies 3 mer CTT 38% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _start=1
                                                                                                                                                                                                               _copies 3 mer CTC 55% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    copies 6 mer ATCAAA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copies 6 mer AACACC 28% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O Copies 2 mer CT 36% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies 6 mer TTCCCC 26% conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Em: AZ639349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6972 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
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ACCESSION
VERSION
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AC112634
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Best Local Similarity
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Mizny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Allen, C., Allen, H., Allen, C., Allen, H., Allen, C., Anyasiabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Cardenas, V., Carter, K., Cavazos, I., Calderon, E., Chen, C., Coyle, M., Calderon, E., Chen, C., Coyle, M., Center, A., Cleveland, C., Coyler, M., Chen, F., Chen, Z., Chu, J., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dedrich, D., Dengon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evyans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, M., Foster, M., Garcia, A., Garra, M., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Karpathy, S., Kelly, S., Hullyk, S., Hume, J., Idebsird, D., Jackson, A., Jackson, A., Hogues, M., Jackson, A., Lebow, H., Levan, J., Idebsird, D., Jackson, A., Longaere, S., Lopez, J., Liu, Y., London, P., Longaere, S., Lopez, J., Liu, J., Lorensuhewa, L., Loulseged, H., Lorgado, R.J., Lu, X., M., J., Lu, X., M
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Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACLIZAS4 230227 bp DNA linear Rattus norvegicus clone CH230-122C23, WORKING DRAFT AC112634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Tandem repeat. Forced join. Gap size estimated be approximately 600bp by restriction digest data." /note="Lx8 repeat: matches 6087..6933 of consensus" /note="Lx8 repeat: matches 5727..5846 of consensus" /note="Lx8 repeat: matches 5727..5846 of consensus" /note="Lx8 repeat: matches 5727..5846 of consensus" /note="1.6.0 copies 1 mer T 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:25072799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence confirmed by mouse whole genome shotgun supercontig data sequenced by the Mouse Genome Sequencing Consortium, contig 199684, version 2." complement(21025. 22191) /note="LIF repeat: matches 59. .591 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14502. 14710

14502. 14710

Inote="L1 MM repeat: matches 6172. .6380 of consensus"

complement (15070. .21003)

Inote="L1F repeat: matches 550. .6618 of consensus"

20673. .20758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not_experimental
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/note="L1_MM repeat: matches 6407. .6587 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="CpG island"
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93.6%;
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Pred. No. 0.2;
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HTG 19-NOV-2002 SEQUENCE.

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Gaps

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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Minorgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plazo, M., Outroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, M., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Shen, H., Steinhe, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walten, L., Walter, F., Wang, G., Waltson, R., Willson, R., Willson, R., Walter, B., Wang, J., Warren, J., Warren, J., Warren, J., Wang, J., Yoon, V., Yu, F., Zhang, S., Zhou, J., Smith, D.R., Holt, R.A., Smith, H.O., Meinstelbe, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265745.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represente a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 230227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Genome Sequencing Consortium.
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                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 230227)
                                                                                                                                                                                                                                                                                        Center project name: GSRQ (enter clone name: CH230-122C3)
Center clone name: CH230-122C3
Center clone name: CH230-122C3
Assembly program: Phrap; version 0.990329
Consensus quality: 218431 bases at least Q40
Consensus quality: 219953 bases at least Q30
Consensus quality: 220995 bases at least Q20
Consensus quality: 22099 bases at least Q20
Estimated insert size: 221147; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
correct as given, however the
                                                                                                                                                                    _data.html)
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AC120625
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COMMENT

JOURNAL, AUTHORS

REFERENCE TITLE

TITLE JOURNAL

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TITLE JOURNAL REFERENCE

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Best Local Similarity
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Rattus norvegicus clone CH230-12B24, WORKING DRAFT SEQUENCE, 3
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 230227: contig of 230227 bp in length.
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clone_end:Sp6
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:lone_end:Sp6"
;600._.6570
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23265453.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the Clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Submitted (99-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 230313)
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_deNOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                        NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                      Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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REFERENCE AUTHORS TITLE

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RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceassar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Ding, Y., Dinh, H., Diyas, K., Bgan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Franadez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garca, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACIII.331.4 GI:30578964
ACIII.391.4 GI:30578964
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway Rattus norvegicus
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Rattus norvegicus clone CH230-145D10, WORKING DRAFT SEQUENCE, 10
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* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 268151)
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224684. .225557
/note="clone_boundary
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226357. .227909
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/mol_type="genomic DNA"
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93.6%;
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Pred. No. 0.2;
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,

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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, B.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F., Poindexter, A., Rose, K., Regier, M.A., Reigh, R.,
Plazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scottl, G., Shatsman, S., Shen, H.,
Sheet, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Sheet, A., Sodergren, E., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Walter, B., Wang, J.,
Waight, D., Waight, R., Willson, R., Wiezzyk, R., Wooden, H., Worley, K.,
Waight, D., Waight, R., Shou, J., Zhou, X., Zhao, S., Dunn, D., von,
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:23268032. The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shortgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct
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Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shotgun sequence only table.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular and Human Genetics, ylor Plaza, Houston, TX 77030, (bases 1 to 268151)
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Center clone name: CH230-145D10
------ Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 249266 bases at least Q40
Consensus quality: 250442 bases at least Q30
Consensus quality: 251941 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor Co
                                                                                                                                                                                                                                                           Center project name: GMEA
                                                                                                                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
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                                                                                                                                                                                                                                                                                                             Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               College of Medicine
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REFERENCE AUTHORS TITLE

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                                                                                                                                                                                                                            44;
                                                   1198 bp
Equus caballus gene encoding alpha
partial.
Y15945
                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGA 47
alpha adrenergic receptor; subtype 28 Equus caballus (horse)
Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                         Y15945.2 GI:6448521
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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264772
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261200
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37382
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clone_end:T7"
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183431. .183726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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268151: contiq
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93.6%;
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Pred. No. 0.2;
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Search completed: February 29, 2004, 22:17:19 Job time: 899 secs
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AUTHORS
TITLE
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Best Local Similarity 90.0%; Pred. No. 0.31;
Matches 45; Conservative 0; Mismatches 5; Indels
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                                                          Revised by [3]
3 (bases 1 to 1198)
Madsen, O.
Direct Submission
Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madsen, O.
Direct Submission
Submitted (16-DEC-1997) O. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
NETHERLANDS
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On Nov 17, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanhope,M.J., Madsen,O., Waddell,V.G., Cleven,G.C., de Jong,W.W. and Springer,M.S.
Highly congruent molecular support for a diverse superordinal clade of edemic African mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                              / CL XYEE - WISS-PROT:077721"

/ db XYEE - "GOA:077721"

/ db XYEE - "GOA:077721"

/ translation - "AIAAVITFLILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAA

DILVATLIIFFSLANELLGYWYERTWCIVLALDVLFCTSSIVHLCAISLDRYWAVT

RALEYNTKRTPRRIKCIILTYWLIAAVISLPFLIYKGDQBCPRGRPQCKLNQBAWYI

LASSIGSFFAPCLIMILVYLRIYLIAKRSHLKGPRAKGGPGCGGSKQPHVPAGASAS

AKLPTVASCLAAAGEANGHSEPTGKKAAFTPEDSGTPALPSSWPALPSSGQDQKKGVC

GASLEEBABEEEEBEEEGGEEGCBEPGALPASPASACSPFLQDPGGSRVLATLRGQV

LLGRGVATAGAQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICP"
                                                                                                                                                                                                                                                                                                                                                                                                                                               (codon start=2
/product="alpha adrenergic receptor subtype 2B"
/protein id="CAA75898.2"
/db_xref="GI:6448522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Equus caballus"
|mol_type="genomic DNA"
|db_xref="taxon:9796"
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Aad436549 Human alp
Aac56583 Human sig
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Ada03065 Mouse Ppp
Adb72803 Mouse Ppp
Adb78803 Mouse Ppp
Aal38337 Complemen
Abg76418 S. Cerevi
Aad55832 Human nuc
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Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR;
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Absoloo39 Human gen
Adb59059 Toxicity-
Adb59059 Toxicity-
Absoloo39 Human yr
Adb59812 Primary r
Abs3973 DNA encod
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Abs39629 CDNA encod
Aca12158 Human Ilun
Abt42404 Toxicity-
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Aak25474 Human b
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                                                                                                                    The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) controlled the site of these and for these and for the sequence includes a general complement of the sequence includes the comprising nucleotide positions 901-909 of (I), a site comprising complement of; and (b) detecting a polymorphic comprising nucleotide positions 901-909 of (I), a site comprising comprising comprising of (IIV) or a site comprising comprising comprising detecting a polymorphic comprising detecting a polymorphic site which correlate the comprising comprising detecting a polymorphic site which correlate to disease and further used to determine whether an individual is at increased comprising detecting a polymorphic site which correlate to disease and combinations of these. In addition, the technique may be used to predict combinations of these. In addition, the technique may be used to predict unitable and combinations of these, comprising and combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or alpha2C agonist (e.g. pracosin, ARC 239, raumolscine, idazoxam, tolazoline, plentolamine and combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or an alpha2B, alpha2A, or alpha2C combinations of these or alpha2C combinations of these or alpha2C combinations of the compression combinations
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                                                                                                          Sequence 1353 BP; 224 A; 458 C; 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting polymorphic site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIGG/)
(SMAL/)
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10-AUG-2000; 2000US-00636259.
19-OCT-2000; 2000US-00692077.
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                                                                    51;
                                                                              Similarity
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DB; AAM52117.
4; Page 144; 163pp; English.
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) SMALL K M.
                                                              ilarity 100.0%;
Conservative 0
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/Note= "sequence includes a 9 nucleotide polymorphic site
at nucleotides 901-909 absent in the alpha-2BAR variant
(AAI99906)"
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Pred. No.
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                                                                                                                                   The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary hat disease (CDD), unstable chromic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine norepinephrine; pennephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                             Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                              New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snapir A, I
Scheinin M,
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                                                       Conservative
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                                                                  100.0%; Score 51;
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T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                  DB 5;
                                                                   00055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Į,
                                                                                 Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koulu M, Pe
Nyyssoenen
                                                      Indels
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RESULT 4
AAQ14151
ID AAQ1
XX AAQ1
AC AAQ1
XC AAQ1
XC Huma
XX Huma
XX Neux
XX Neux
XX Homc
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                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                    The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor gene
                                                                                                                                                                                                                                                                 Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD44389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD44389 standard;
 Homo sapiens
                       Neurotransmission;
                                                                     06-JAN-1992
                                                                                          AAQ14151;
                                                                                                                 AAQ14151 standard;
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001FI-00000323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; hypertension; alpha-2B-adrenoceptor;
hypertension; hypotensive; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human alpha-2B-adrenoceptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JURI-)
                                                                                                                                                                         880
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-667063/71
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                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JURILAB
                                                                                                                                                                         GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 930
                                              N
                                                                                                                                                                                                                     Conservative
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                                                                     (first
                                              beta
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                 DNA;
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                       adrenaline;
                                             adrenergic
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                                                                   entry.
                                                                                                                                                                                                                               100.0%;
                                                                                                                 2064
                                                                                                                                                                                                                                         .04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human alpha-2B-adrenoceptor
                                                                                                                                                                                                                     <u>,,</u>
                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                               Score 51;
Pred. No.
                                              receptor
                       epinephrine; NGC-alpha2beta;
                                                                                                                                                                                                                     Mismatches
                                              gene
                                                                                                                                                                                                                                 0.00055;
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                                                                                                                                                                                                                                            <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR; antihypertensive;
                                                                                                                                                                                                                                          Length 1353;
                         88
                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                    testing the human alpha
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AAT59499
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Best Local (
                                  Hartig PR,
                                                                                               30-OCT-1989;
30-MAY-1991;
                                                         (SYNA-) SYNAPTIC PHARM CORP
                                                                                                                                               22-OCT-1992;
                                                                                                                                                                                21-JAN-1997.
                                                                                                                                                                                                                US5595880-A.
                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                               Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; signal transduction; neurotransmitter; ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                              Human alpha-2b adrenergic receptor genomic DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT59499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT59499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone NGC-alpha2beta was isolated from a human spleen genomic library screening with a fragment of the human 5-HTIA receptor gene. The gene be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2064 BP; 319 A; 696 C; 659 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated DNA encoding human adrenergic receptor - acids encoding alpha, 2-beta adrenergic receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR14149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1989;
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                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAAGGAAGAGGAGGAGGAAGAAGAGTGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEUROGENETIC CORP.
                          Weinshank RL,
                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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                                                                                         89US-00428856
91US-00707604
                                                                                                                                          9208-00965040
                                                                                                                                                                                                                                           Location/Qualifiers
288. .1751
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 2064
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288. .1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB Pred. No. 0.0 0; Mismatches
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r detecting ;
                                                                                                                                                                                                                                                                                                                                              epinephrine;
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drugs.
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RESULT 6
ACA5583
ID ACA5
XX ACA5
XX ACA5
XX ACA5
XX Huma
XX Huma
XX Huma
XX Huma
XX Homo
XX Homo
XX Ion
PN Us85
XX Jo-J
XX Jo-J
XX INC
PR 30-J
XX INC
PR 30-J
XX UNC
PR 30-J
XX INC
PR 10-J
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PR 10-J
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Best Local S
Matches 51
                                                                                                                                                                                                              Au-Young J,
                                                                                                                                                                                                                                                                               30-JAN-1998;
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number
                                                                                                                                                                           Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma immunopathy; AIDS; asthma; neuropathy; Alzheimer's di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6500938-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human signalling pathway polynucleotide probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAW1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 16 be fragment of the human 5 encoding the alpha-2B adrenoceptor gene. Plasmid pNGC-alpha-2B comprising DNA have been adapted to allow prodm. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in bound to, the alpha-2B adrenoergic receptor. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-107576/10.
P-PSDB; AAW11804.
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                                                                                                                                    SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAAGAGTGT
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                                                                                                                                                                                                                                                                                                                                    Seilhamer JJ;
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Conservative 0;
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Pred. No. 0.0005(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenocarcinoma; leukaemia;
Alzheimer's disease; micro
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hes 0;
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RESULT 7
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Best Local
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; spliepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000; 2000US-0257144P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200261087-A2
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                                                                                                                                           2003-046718/04.
DB; ABP81780.
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                                                                                                                                                                                                                                                                                                           LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGT 51
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                                                                                                                                                                                                                                            Rough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or a vidity for a particular GPCR. (I) can be used as GPCR modulators and in Gqne therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting an antibodies. The peptides and antibodies are also useful for detecting the gresence or absence of corresponding GPCRs. The antigenic peptides for CC regeneration-related diseases, immunological and designing drugs for treating immune-related diseases, growth-related diseases, cell cc atherosclerosis, bacterial, fungal, protozoan or viral infections, conceroarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory asthms theorements, mental retardation, memory antiper antiper of the protocode of the protocode of the parkinson's disease, multiple sclerosis, pain, psoriasis, memory asthms theorements, mental retardation, memory antiper antiper of the protocode of the protocode of the parkinson's disease, multiple sclerosis, pain, psoriasis, memory asthms theorements, mental retardation, memory antiper antiper of the protocode of the protocode
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Matches
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New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3274 BP;
                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS68926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS68926 standard; cDNA; 291 BP
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                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001.
                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                            2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
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                                                                         ABG04739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel human diagnostic protein #4730
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                                                                                                                                         Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; Di
100.0%; Pred. No. 0.
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3274;
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    mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
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The invention relates to isolated polynucleotide sequences. (I) is useful as hybridisation probes,

Claim 1; SEQ ID NO 4730; 103pp; English.

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CC sequences. (I) Is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polymerase chain CC in diagnostics as expressed sequence tags for identifying expressed cactivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore mapping, CC quesful for generating antibodies against it, detecting or quantitating a cc upplement. (II) and its binding partners are useful in medical imaging CC involving aberrant protein expression or biological activity. The CC involving aberrant protein expression or biological activity. The CC adaptostics forensics, gene mapping, identification of mutations CC and to produce other types of data and products dependent on DAM and CC and to produce other types of data and products dependent on DAM and CC coding sequences. AAS64197-AAS94564 represent novel human diagnostic CC electronic format directly from WIPO a cc. fip. wipo.int/pub/published nor appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                  LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             responsible for genetic disorders or other traits and to assess
                                                                                 bone development, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                      Query Match
                            This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. disgnostic acid molecules, proteins and antibodies can be used in the diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and in the method of the invention
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                                                                                                                                                                                                                                                          Example 3; Page 69-97; 391pp; German.
                                                                                                                                                                                                                                                                            Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders.
                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27+MAR-1998; 98DE-01013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9950284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine LOBO genomic DNA fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ23891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel nucleic acids (I, designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic acidity. It is a proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ23891 standard; DNA; 49999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
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                                                                                                                                                                                                                                                                                                                                                                                            Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-EP002055
                                                                                                                                                                                                                                                                                                                                                                                        Невя J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                  Aigner T,
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                Wirth
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Query Match Best Local Similarity

44;

Conservative

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Pred. No. 0.11 0; Mismatches Score 41.6; DB 5; Pred. No. 0.11;

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48

Length 291; Indels

81.6%; 91.7%;

Sequence 291 BP; 129 A; 22 C; 112 G; 28 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

48 0

Gaps

0,

RESULT 9
AAZ23896
ID AAZ2:
XX AAZ2:
XX AAZ2:
XX AAZ2:
XX AAZ2:
XX LOBO
KW LOBO
KW CHAR HOSO
KW CHAR HOSO
XX HOSO
PM 07-0
XX PF 26-M
XX HOSO
PM (ROS:
XX WOSO
PM WOSO
P

Murine LOBO homologue genomic DNA fragment 2.

25-JAN-2000 (first entry)

AAZ23896;

AAZ23896 standard; DNA; 49999

₽P

Nucleic acids encoding proteins which influence for treating and studying bone disorders.

WPI; 1999-601320/51

Rosenthal A,

Rump A,

Невв J,

Aigner T,

Wirth

(ROSE/) ROSENTHAL A.

27-MAR-1998; 26-MAR-1999; 07-OCT-1999 W09950284-A2

98DE-01013799. 99WO-EP002055.

Example 3; Page 161-189; 391pp;

Score 41.6;

DB 2;

Length 49999

91.7%;

Pred. No.

0.12;

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ADA66349/c
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                                                                                                This invention relates to a novel recombinant carcinoma-associated (CA) CC nucleic acid comprising a fully defined genomic, mRNA or coding sequences of mouse Rorc gene or human RORC gene, mouse mCG15938 or human gene BAT1, CC mouse Iqgapl gene or human IQGAP1 gene, mouse EZF29 gene or human CC hCG27579 gene, mouse KCG1910 gene or human KCNV9 gene, mouse PD93CC gene or human RCNV9 gene, mouse PD93CC gene or human CC concer cells, preferably lymphatic, breast, prostate or pitchelial cells. CC carcinoma-associated proteins (CAP) may have cytostatic activity and the CR gequences of the invention may enable the use of gene therapy or a CC development of an anticancer vaccine. The refore the invention may be CC useful for diagnosis and treatment of carcinomas, especially lymphoma CC carcinoma, breast cancer and prostate cancer. The CA genes may also be CC useful as DNA vaccines and for generating animal models of carcinomas. CC The present sequence is that of the mouse Pp3Cc gene genomic DNA CCC sequence of the invention.
 Best Loc
Matches
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Matches 44; Conserv
                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma-associated gene; CA gene; Rorc gene; mCG15938 gene; BAT1 gene; Iqgap1 gene; IQGAP1 gene; Zpf29 gene; hCG27579 gene; Kcnj9 gene; KCNJ9 gene; Ppp3cc gene; PPP3CC gene; mCG910 gene; hCG27579 gene; cancer cell; lymphatic cell; prostate cell; prostate cell; epithelial cell; carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer; vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer; prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Ppp3cc.
                                                                    Sequence 68230 BP; 18765 A; 14103 C; 14728 G; 20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 110-120; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant carcinoma-associated nucleic acid, useful for evaluating the effect of a candidate carcinoma drug, and for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-569168/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrie DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2002; 2002WO-US041776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003053224-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Ppp3cc gene genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10399
 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Engelhard
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                  81.6%;
91.7%;
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 <u>..</u>
                Score 41.6; DB Pred. No. 0.12;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                8
4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                Length 68230;
 Indels
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GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG 48

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RESULT 12
ADA03065/c
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                                                                                                                                                                                                       The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADA)1482-ADA03094), and to CC carcinobinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC cA nucleic acid, a polypeptide (especially an antibody) that specifically compasses to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host CC pathogenic trans-acting viral genes, meaning that cancer incidence is a Cd irect consequence of the effects of proviral integration into host CC pathogenic or a propensity to carcinoma by determination of the sequence CC carcinoma (specially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence CC acides, proteins and antibodies are also useful as CC therapeutic agents and in screening and evaluating drug candidates. The CC present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this CC patent did not form part of the printed specification, but was obtained crift electronic format directly from WIPO at
                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                        Sequence 68233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1583; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Ppp3cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA03065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA03065 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2002; 2002WO-US041414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WQ2003057146-A2
                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58099
  44;
                                                                                               Similarity
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma associated gene, SEQ ID NO:1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                        BP;
                                                                                                                                                        18767 A; 14103 C; 14729 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                               81.6%;
91.7%;
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                                                                                               Score 41.6;
Pred. No. 0.
                                                                             Mismatches
                                                                                               .12;
                                                                             4.
                                                                                                                                                        20634 T; 0 U; 0 Other;
                                                                                                               Length 68233;
                                                                               Indels
                                                                               0
                                                                               Gaps
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04-DEC-2003 ADB72803;

(first

entry)

ADB72803 standard; DNA; 68233

ВP

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RESULT 14
AAL38337/c
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Matches
                                                                                                                                                                                                                                                                                                      Query Match
Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
                                                                                                    Complementary
                                                                                                                            15-AUG-2002
                                                                                                                                                    AAL38337;
                                                                                                                                                                          AAL38337
                                                                                                                                                                                                                                                                                                                         The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                        Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00937722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2001; 2001WO-US051291.
                                                                                                                                                                                                                                   88099
                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Ppp3cc gene
                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant nucleic acid, useful for treating carcinomas, lymphomas,
cers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                 standard; DNA; 215980 BP
                                                                                                                                                                                                                 ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 631; 2304pp; English.
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                           Conservative
                                                                                  strand of a genomic sequence encoding a mouse NgR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engelhard
                                                                                                                                                                                                                                                                                  81.6%;
91.7%;
                                                                                                                                                                                                                                                                         °,
                                                                                                                                                                                                                                                                                Score 41.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                               .12;
                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                         9,
                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                     Length 68233;
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RESULT 15
ABQ76418/c
ID ABQ76418 standard;
                         SAXFXEX
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                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a Nogo receptor homologue polypeptide, NgR2 or NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT comprising a 20, 461 or 392 amino acid sequence, all given in the generation. The NgR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system (CNS) cuseful for treating the neuron NgR3 or its antibody, and for treating cerebral injury, MgR3 or a vector comprising NgR3 is compressing NgR3 is untiliple selectors of injury, stroke, compressing NgR3 is useful for inducing an immune response in a compression of interacting, regulatory proteins the nucleotide sequences of the invention are useful for screening for RFLP associated compression of the invention are useful for screening for RFLP associated compression and compression an
                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                         Query Match
S. cerevisiae BAX-associated cDNA fragment
                                                  21-NOV-2002
                                                                                        ABQ76418
                                                                                                                                                                                                                                                                                                                         Sequence 215980 BP; 56872 A; 50995 C; 50240 G; 54437 T; 0 U; 3436 Other;
                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 16; Page 219-275; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal
                                                                                                                                                                                                                 19661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strittmatter SM, Cate RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000US-0238361P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2001; 2001WO-US031488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic a murine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200229059-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krabbe's disease; immune; bait transgenic animal; unregulated
                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                        Conservative
                                           (first entry)
                                                                                                               CDNA; 1721
                                                                                                                                                                                                                                                                                          81.6%;
91.7%;
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                                                                                                                                                                                                                                                                                      Score 41.6; DB Pred. No. 0.13;
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                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JWY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; genetic mapping; gene therapy;
cellular growth; cancer; tumour; mouse;
                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                              Length 215980;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                         Gaps
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SEQ

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RESULT 16
AAD55832
ID AAD55
XX
AC AAD55
XX
DT 07-AU
XX
DE Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel nucleic acid representing a synthetic CC Bax gene. The Bax gene of the invention is useful for identifying Bax-CC resistant yeast or fungi, identifying, or obtaining and identifying CC Candida spp. sequences that are differentially expressed in a pathway CC eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the CC invention have cytostatic, fungicide; immunosuppressive, virucide and CC vasotropic activity and can be used in vaccines or for gene therapy. The city of the CC isolated nucleic acids, polypeptides, pharmaceutical compositions, CC antisense molecules and antibodies are useful as medicaments or in CC preparing a medicament for treating, preventing and/or alleviating such as cancer, or for preventing apoptosis in certain diseases. The compounds CC as cancer, or for preventing apoptosis in certain diseases. The compounds CC preparing a medicament for modifying the endogenic flora of humans and CC conter mammals. The vaccine is useful for immunising against yeast or CC ischaemia, diseases related diseases include autoimmune disease, CC ischaemia, diseases related with viral infections or neurodegenerations. CC this sequence represents a polynucleotide associated with the Bax gene described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 43
                                                              07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-2000; 2000EP-00870318
04-JAN-2001; 2001EP-00870002
09-JAN-2001; 2001EP-00870003
                                                                                                                                                                                   AAD55832 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 36; Fig 1; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2001; 2001WO-EP015398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-667002/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                               GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eberhardt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.6%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 400 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 G; 479 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reekmans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                       585
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Human nucleic acid associated

protein (NAAP) -3 cDNA.

밁

930 GAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGA

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Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001US-0305089P.
12-JUL-2001; 2001US-0305104P.
13-JUL-2001; 2001US-03053259.
13-JUL-2001; 2001US-0305390P.
19-JUL-2001; 2001US-0306694P.
20-JUL-2001; 2001US-0306614P.
27-JUL-2001; 2001US-0308170P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yde H, Baughn MR, I
Ramkumar J, Li JX,
Burford N, Elliott V
Barroso I, Tran B,
                                                                                                                                                                                                                                  epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. It is also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NAAP. The NAAP or its fragments are useful in screening compounds for which acts as their agonist or antagonist. The microarray is useful in monitoring or measuring protein-protein interactions, drugter interactions, and gene expression profiles. NAAP DNA is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       in diagnosing, treating and preventing diseases or conditions as with the decreased expression or overexpression of NAAP, such as proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; developmental disorder; antiinflammatory; neuroprotective; thyromimetic; Cushing's syndrome; infection; gene therapy; cytostatic; anticonvulsant; cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
                                                                                                                                                            Sequence 2663 BP; 875 A; 497 C; 715 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acid associated proteins (NAAP) and their corresponding nucleic acid sequences. The invention is usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nucleic acid associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                            therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-221732/21.
DB; AAE37016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Page 232;
1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGA 47
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
237. .2444
/*tag= a
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                                                                                                                                                                                                               present sequence is human NAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nardson TW, Warren BA, Grif

Marting BM, Lal PG, Lu

Marting BM, Duggan BM, Sa

Lu VS, Ison CH, Ding L, Bd

Malla NK, Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260pp; English
                                                                           79.6%;
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                                                                           Score
Pred.
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                                                                              40.6;
No. 0
                                                                              DB
.21;
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, Lu DAM, Forsyth
M, Sanjanwala MM,
L, Borowsky ML, Y
AJA, Nguyen DB, L
                                                                                                                                                                                                                    CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forsythe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yao MG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee EA;
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RESULT 17
AADO4761
ID AADO4761
AXX AADO44
AXX AADO4
AXX AADO4
AXX AADO4
AXX Human
XXX Homo
XXX Homo
XXX Homo
XXX Homo
XXX Homo
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                                                                                                                                                                                                                                          The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat celement (amino acids 298-309) off 12 glutamates, in an acidic stretch of CC 18 amino acids (amino acids 294-311), located in the third intracellular three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR CC gene is located on chromosome 2. Alpha2-AR mediate many off the CC gene is located on chromosome 2. Alpha2-AR mediate many of the CC ghispiological effects of the catecholamines, norepinephrine and CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating CC disease involving vascular contraction of coronary arteries and a CC clinically expressed as coronary heat disease (CHD), unstable chronic CC disease involving wascular contraction of coronary arteries which is clinically expressed as prinzmetal's variant correction of acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                                                                   Query Match
Best Local S
Matches 42
                                                                                                                                                                                                     Sequence 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 24-26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salonen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snapir A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cardiant; gene therapy, alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha2B-adrenoceptor (alpha2B-AR) variant
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42; Conser
GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAAGAA 45
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                                                                                              Conservative
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                                                                                                                                                                                                  B₽;
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/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
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                                                                                                              78.8%;
93.3%;
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Tuomainen T,
                                                                                 Score 40.2; DB
Pred. No. 0.26;
0; Mismatches
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                                                                                                                                                                            400 G; 266 T; 0 U; 0 Other;
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T, Lakka
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                                                                                   <u>ں</u>
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                                                                              Indels
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Nyyssoenen
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                                                                        Gaps
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RESULT 19
ABX90802
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AAD44388
                                                                                                                                                                                            Query Match
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  Murine gene
                        07-MAY-2003
                                                                   ABX90802
                                                                                                                                                                                                         Sequence 1344 BP; 219 A; 459 C; 400 G;
                                                                                                                                                                                                                                  The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of selecting for clinical drug trials testing the antihypertensive effect of selecting the present sequence is human alpha
                                                                                                                                                                                                                                                                                                                                              Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 24-26; 35pp; English
                                                                                                                                                                                                                                2B-adrenoceptor variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Salonen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002; 2002WO-FI000113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (JURI-) JURILAB
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; hypertension; alpha-2B-adrenoceptor; A hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                Local
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                                                                                                                            980
                                                                                                                                                                                                                                                                                                                                                                                           2002-667063/71.
DB; AAE26633.
                                                                                                                                                                     42;
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                                                                                                                                                                              Similarity
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                                                                  standard;
                                                                                                                 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGTGTGAA 924
                                                                                                                               GAGGATGAAGCTGAAGAGGAGGAAGAAGGAGGAGGAGGAGGAAGAA 45
trapped sequence
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                                                                                                                                                                   Conservative
                      (first entry)
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1. .1344
                                                                  CDNA; 223
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                                                                                                                                                                            78.8%;
93.3%;
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                                                                                                                                                                          Score 40.2;
Pred. No. 0
                                                                                                                                                              Mismatches
                                                                                                                                                                                                     266 T; 0 U; 0 Other;
                                                                                                                                                                          . 26;
                                                                                                                                                                                    DB
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                                                                                                                                                                                 Length 1344;
                                                                                                                                                             Indels
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(GTS)

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ARS75432
ID AAS75
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XX Human
KW food
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                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel murine cDNAs produced using gene trapped sequences (GTSs) are individually identified novel genes, and are useful in functional genomic analysis, in the discovery and development of new therapeutic and diagnostic agents, for gene discovery, for diagnostic gene expression analysis, for cross species hybridisation analysis, and for genetic manipulations such as antisense inhibition or gene targeting. The polynucleotides of the invention are also useful for isolating cDNAs, genomic clones or full-length genes/polynucleotides, or their homologues, genomic clones or full-length genes/polynucleotides, or their homologues, heterologues, paralogues or orthologues, that are capable of hybridising to one or more of the new murine polynucleotide sequences. The polynucleotides are also useful for identifying the coding regions of the murine genome, and as hybridisation probes. ABX90657-ABX91862 represent the murine GTSs of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; mouse; gene trap technology; gene trapped sequence; GTS; gene thentification; functional genomic analysis; gene discovery; gene expression analysis, cross species hybridisation analysis; antisense inhibition; gene targeting; gene; ss.
                                                                  DNA encoding
                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 223 BP; 64 A; 31 C; 65 G; 48 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic agents, for diagnostic gene expression analysis or for genetic
            Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                         AAS75432 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    electronic format directly from the seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 146; 29pp;
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(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                 43,
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                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                              GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAAGAG
                                                                novel human diagnostic protein #11236.
                                                                                                     (first entry)
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                                                                                                                                                                       cDNA;
                                                                                                                                                                                                                                                                                                                                               78.4%;
89.6%;
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Pred. No.
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د.
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                                forensic;
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RESULT 21
ABQ98152/c
ID ABQ981
XX
AC ABQ981
XX
DT 30-OCT
XX
MOUSE
XX
KW MOUSE;
XW develc
XX
OS Mus sg
XX
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                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                  reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies are useful for generating antibodies of the detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                            Mouse; ES cell;
development diso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                 Mus sp
                                                                                                 Mouse ES cell related cDNA SEQ ID NO 1420.
                                                                                                                                 30-OCT-2002
                                                                                                                                                                                                  ABQ98152 standard; cDNA; 234 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 11236; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ INC.
                                                                                                                                                                                                                                                                                  ell; gene trapped
disorder; cell d:
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                BP; 117 A; 9 C;
                                                                                                                                 (first entry)
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89.6%;
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                                                   ed sequence; GTS;
differentiation of
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                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                9 T;
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                                                   gene expression;
disorder; gene; s
                                                                                                                                                                                                                                                                                                                                                 <u>ن</u>
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US2002081668-A1

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RESULT 22
ABX90780
                                                                                                                                                                                                                                                             The invention relates to isolated murine polynucleotides (I) comprising a CC contiguous stretch of at least about 60 nucleotides of a sequence CC (AB096733-AB098191) chosen from 1461 OMNIBANK gene trapped sequences CC (AB096733-AB098191) chosen from 1461 OMNIBANK gene trapped sequences CC polynucleotide sequences by comparing them to the novel gene sequences CC The novel genes and cells are useful in functional genomic analysis and continuous period of the novel gene sequences. CC and methods. (I) is useful for identifying the coding regions of the CC murine genome, to isolate cDNAs, genomic clones or full-length cC genes/polynucleotides or homologues, heterologues, paralogues or under stringent conditions. (I) can be incorporated into a phage display CC capable of binding an amino acid sequence encoded by an oligonucleotide capable of hybridising to one or more of the GTSs capable of binding an amino acid sequence encoded by an oligonucleotide temporal in arrays, such as gene chips, to identify and characterise CC antisense inhibition and gene targeting. Decreasing the level of expression of (I) and/or down regulating the level of expression of (I) and/or down regulating the level of groteins encoded by (I) is useful for treating development and cell corm part of the princed specification, but was obtained in CC electronic format directly from USPTO at
                                                                                                                                                                                                                  Query Match
Best Local S
Matches 43
     Murine; mouse; gene trap technology; gene trapped sequence; GTS, gene identification; functional genomic analysis; gene discovery;
                                                      Murine gene
                                                                             07-MAY-2003
                                                                                                                 ABX90780 standard;
                                                                                                                                                                                                                                            Sequence 234 BP; 41 A; 64 C; 39 G; 87 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 1420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel murine polynucleotides that individually identify novel genes which a retroviral gene trap vector has been integrated, useful in genomic analysis and in discovery, development of therapeutic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-626541/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FRIE/) FRIEDRICH G.
(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1998;
01-DEC-1999;
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43; Conser
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                                                     trapped
                                                                         (first
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                                                                                                                CDNA; 330
                                                  sequence
                                                                       entry)
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99US-0168270P.
                                                                                                                                                                                                                    78.4%;
89.6%;
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                                           (GTS) SEQ ID No 124.
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                                                                                                                                                                                                                   Score 40;
Pred. No.
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RESULT 23
ACD13226
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Best Local
                                                                                        13-AUG-2003
                                                                                                             ACD13226;
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CC The present invention relates to novel murine cDNAs produced using gene CC individually identified novel genes, and are useful in functional genomic CC analysis, in the discovery and development of new therapeutic and CC analysis, for cross species hybridisation analysis, for cross species hybridisation analysis, for cross species hybridisation analysis, and for genetic committees of the invention are also useful for isolating cDNAs, CC polymucleotides of the invention are also useful for isolating cDNAs, CC to one or more of the new murine polymucleotides or their homologues, comparison of the new murine polymucleotide sequences. The murine grown, and as hybridisation probes. ABX90657-ABX91862 represent CC did not form part of the printed specification, but was obtained in CCC secondard directly from the USPPTO web site at
NOVX; autoimmune disease; allergy; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; multiple sclerosis; addiction; anxiety; pain; diabetes; glomerulonephritis; obesity; systemic lugus erythematosus; asthma; scleroderma; pancreatitis; graft versus host disease; ulcer; anaemia; cancer; trauma; infection; cardiomyopathy; atherosclerosis; hypertension; AIDS; Crohn's disease;
                                                                                                                                                                               cDNA encoding novel human protein NOV37a.
                                                                                                                                                                                                                                                                                                                           ACD13226 standard; cDNA; 1173 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 330 BP; 123 A; 59 C; 91 G; 54 T; 0 U; 3 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic agents, for diagnostic gene expression analysis or for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRIE/) FRIEDRICH G.
(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2000; 2000US-00728444.
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antisense inhibition; gene targeting; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-288124/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.4%;
89.6%;
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Pred. No. 0
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The invention describes an isolated NOVX polypeptide (I) comprising a cc sequence selected from a sequence (S1) of 1121, 635, 299, 1720, 176, 583, CC 214, 395, 1098, 134, 427, 1333, 407, 806, 804, 1253, 382, 1045, 284, 496, CC 506, 759, 390, 133, 215, 240, 1069, 116, 439, 1138, 477, 316, 269, 219, CC specification, and the mature form of S1. (I) is useful for treating or preventing a pathology associated with (I) in a subject, preferably CC human, or for identifying an agent that binds to (I), where the agent is cendding (I) or an anti-(I)-antibody (V) is useful treating or preventing constrained with (I) in a subject, preferably cc encoding (I) or an anti-(I)-antibody (V) is useful treating or preventing disease, stroke, parkinson's disease, Huntington's disease, multiple cc sclerosis, addiction, anxiety, pain, diabettes, glomerulonephritis, consisted assays, pancreatitis, obesity, ulcers, anaemia, cancer, trauma, viral, cc disease, pancreatitis, obesity, ulcers, anaemia, cancer, trauma, viral, cc disease, conservable, conservab
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07-JUN-2001; 2001US-029575P.
11-JUN-2001; 2001US-0297414P.
12-JUN-2001; 2001US-0297567P.
15-JUN-2001; 2001US-0297567P.
16-JUN-2001; 2001US-0299330P.
19-JUN-2001; 2001US-0299330P.
21-JUN-2001; 2001US-029930P.
22-JUN-2001; 2001US-0300177P.
26-JUN-2001; 2001US-03001530P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
03-JUL-2001; 2001US-0301550P.
03-JUN-2001; 2001US-0301550P.
17-SEP-2001; 2001US-0318727P.
27-SEP-2001; 2001US-0358814P.
03-JUN-2002; 2002US-0358814P.
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Padigaru M, I
Patturajan M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as autoimmune disease, allergies, Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease or multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-2002;
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Li L, Pena
4, Stone DJ;
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Gangolli EA, Ve
In L, Anderson DW,
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EA, Vernet CAM;
rson DW, Edinger (
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RESULT 24
ACD13227
ID ACD13227
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Matches
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19-JUN-2001; 2001US-029930P.
21-JUN-2001; 2001US-039949P.
22-JUN-2001; 2001US-0300177P.
26-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
28-JUN-2001; 2001US-0301550P.
27-SEP-2001; 2001US-031563P.
27-SEP-2001; 2001US-031563P.
27-SEP-2001; 2001US-031563P.
                                                                                                                                                                                   Zerhusen BD,
Gerlach VL,
Padigaru M,
Patturajan M
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06-JUN-2001;
06-JUN-2001;
07-JUN-2001;
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12-JUN-2001;
15-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; Huntington's disease; multiple sclerosis; addict anxiety; pain; diabetes; glomerulonephritis; obesity; systemic lupus erythematosus; asthma; scleroderma; pancreatitis; graft versus host disease; ulcer; anaemia; cancer; trauma; infection; cardiomyopathy; atherosclerosis; hypertension; AIDS; Crohn's disease; acquired immunodeficiency syndrome; chromosomal mapping; tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1173 BP; 326 A; 290 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-2003
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                                                                                                                                                                                                                                                                                                       (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forensic biology; predictive medicine; gene therapy; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                    2003-140585/13.
DB; ABO07153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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2001US-0297567P.
2001US-029852BP.
2001US-0299133P.
2001US-0299330P.
2001US-0299340P.
2001US-0300177P.
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2001US-0296418P
                                                                                                                                                                                                           Baumgartner
Li L, Pena
                                                                                                                                                                                                                                                                                                                                                     2002US-00161927
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                                                                                                                                                                                                                                                              Kekuda
                                                                                                                                                                                        Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 1178
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89.6%;
                                                                                                                                                                                                           Spytek KA,
JC, Guo X,
CEA, Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein NOV37b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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Pred. No. 0.29
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 G;
                                                                                                                                                                                                           Shenoy SG, Mille
Gangolli EA, Ve
n L, Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                    Miller CE, HJair
A, Vernet CAM;
on DW, Edinger SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                                         Hjalt T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   addiction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as autoimmune disease, allergies, Alzheimer's disease,

Parkinson's

disease,

Huntington's

disease

9

multiple

sclerosis

Claim

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RESULT 25
AAC38547
ID AAC38
XX AAC38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The invention describes an isolated NOVX polypeptide (I) comprising a CC 214, 395, 1098, 134, 427, 133, 407, 806, 804, 1253, 382, 1076, 789, 390, 133, 215, 240, 1069, 116, 439, 1138, 477, 316, 269, 219, CC 305, 406, 460, 365, 380, 829 or 326 amino acids fully defined in the CC preventing a pathology associated with (I) in a subject, preferably CC acilular receptor or a downstream effector. (I), where the agent is CC encoding (I) or an anti-(I)-antibody (V) is useful for treating or CC disorders or syndromes such as autoimmune disease, altergies, Alzheimer's CC systemic lupus erythemacrosus, asthma, scleroderma, graft versus host CC disease, pancreatitis, obesity, ulcers, analy, atherosclerosis, disease, pancreatitic infections, cardiomyopathy, atherosclerosis acquired immunodeficiency syndrome (AIDS) or Crohn's CC disease. (I), (II) or (V) is useful in screening assays, detection assays cedicine (e.g., chromosomal mapping, tissue typing, forensic biology), predictive curials and pharmacogenomic), and in methods of treatment (e.g., dagnostic assays, prognostic assays, monitoring clinical condulate Novx activity. This sequence encodes a novel human Nov protein
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Best Local S
Matches 43
                                                   25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

11-APR-1999

23-APR-1999

23-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Page 204; 408pp; English.
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43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 1956
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                                           99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-01267854P.
99US-0127462P.
99US-0127462P.
99US-0128234P.
99US-0129845P.
99US-0130047P.
99US-01300449P.
99US-0130510P.
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89.6%; Pred. No. 0.29
tive 0; Mismatches
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0.29;
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د.
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28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
11-MAY-1999;
11-JUN-1999;
11-JU
99US 0132486P

99US 0132487P

99US 0132487P

99US 0134218P

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99US 0139458P

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Best Loc
Matches
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28-0CT 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungicide; cancer; cor
The invention relates to novel pessential genes of Aspergillus the invention are used to treat
                                                                                                New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                        Jiang
                                                                                                                                                                                                                                                                           23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-033899P.
31-AUG-2001; 2001US-0316362P.
                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2002;
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                                                                                                                                                                                                                                           ELITRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
                                                                Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fumigatus
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                                                                  English.
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Pred. No. 0.29
0; Mismatches
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purified or isolated nucleic acids of fumigatus. The isolated nucleic acids of or prevent infections by a pathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
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20-JUL-1999 21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 24-JUL-1999 25-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 28-JUL-1999 29-AUG-1999 29-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG

99US-0144844P
99US-0145086P
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99US-0145145P
99US-0145218P
99US-0146386P
99US-0147303P
99US-01477303P
99US-0151066P
99US-0151303P
99US-01518039P
99US-0159331P
99US-0159333P
99US-0159333P
99US-0159333P
99US-0159333P

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RESULT 27
                                                                                                                                                                                                         23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC subject (e.g. cancer), to prevent or contain contamination of an object (e.g. cancer), to prevent or contain contamination of an object CC by A. funigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. funigatus. The polymucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC expressing invade or reside, for comparing with the pathogenic CC similar biochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify duplicated genes or paralogues having the same or potential orthologous essential or virulence genes, for selecting and CC antigen to raise anti-DNA antibodies or to elicit antipodies as an CC with which binding occurs or identify ing polymucleotides encoding the other protein CC interaction. The polypoptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively constituses in which pathogenic organism invade or to solate correlative receptors or ligands in the case or virulence correct. This polymucleotide sequence represents one of the essential correction such pathogenic organisms or to elicit another immune could be protein in biological fluids, as a marker for contents. This polymucleotide sequence represents one of the sesential correlative receptors or ligands in the case or virulence correction. The polymore or content is searched or reside, and to content of the polymucleotide sequence represents one of the essential corrections of the invention.
                                  New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                    Disclosure; Page; 175pp; English
                                                                                                                                                         Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                        (ELIT-)
                                                                                                                                                                                                                                                                                                       23-APR-2002; 2002WO-US013142
                                                                                                                                                                                                                                                                                                                                                                          WO200286090-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus fumigatus essential gene #3212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABT20854 standard; DNA; 2367 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism sucn ...
"whiect (e.g. cancer),
                                                                                                                       2003-093124/08.
                                                                                                                                                         'n
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                                                                                                                                                                                ELITRA PHARM INC.
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                                                                                                                                                   Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2367 BP; 630 A; 644 C; 681 G; 412 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%;
89.6%;
                                                                                                                                             Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
                                                                                                                                        Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No. 0.29;
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                                                                                                                                   Lemieux
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RESULT 28
ABK65237
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                                                                                                                                                                                                                                22-AUG-2000;
16+NOV-2000;
18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                              (CREE/)
                                                                                                                                                           (MEND-)
                                                                                                                                                                                                                                                                                                                                         22-AUG-2001; 2001WO-US026189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200215675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA encoding a transcription factor #89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK65237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK65237 standard; cDNA; 2663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2367 BP; 630 A; 644 C; 681 G; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEARD J.
JIANG C.
KEDDIE J.
                                                                     MENDEL BIOTECHNOLOGY INC.
PILGRIM M.
CREELMAN R..
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                       2000US-00713994.
2001US-00837944.
                                                                                                                                                                                                                                                                                   2000US-0227439P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB Pred. No. 0.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indelg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 29
ACD98382
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant polymucleotide is used for producing a plant having a modified trait, the method comprising selecting a polymucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polymucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower sensecence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information. The isolated or defined sequences given in the specification. The isolated or
                                              Arabidopsis thaliana.
                                                                            Plant; 88; gene; transcription factor;
plant breeding; pathogens resistance; pathogens
                                                                                                                              A. thaliana disease tolerance transcription factor cDNA, G1089
                                                                                                                                                                   23-SEP-2003
                                                                                                                                                                                                                                   ACD98382 standard; cDNA; 2663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding an Arabidopsis thaliana transcription factor, complements, fragments, or related polynucleotide with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 388-393; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated or recombinant polynucleotide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pilgrim M, Creelman
Adam L, Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ADAM/)
(RATC/)
(REUB/)
(RIEC/)
(YUGG/)
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                                                                                                                                                                                                                                                                                                                         865
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) RATCLIFF O.
) REUBER J L.
) RIECHMANN J L.
) YU G.
) PINEDA O.
                                                                                                                                                                                                                                                                                                                                                       1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                         78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reuber JL,
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uber JL, Riechmann JL, Yu G,
                                                                              resistance; pests;
                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         0.29;
                                                                                                disease resistance; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2663;
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                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         their variants,
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Pineda O;
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US2003046723-A1

RESULT 30 ADD30227

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                                                                                                                                                                                              CC polynucleotide that alters the plant's disease tolerance or resistance CC when compared with the same trait of another plant lacking the CC recombinant polynucleotide. The recombinant polynucleotide comprises a CC consecutive amino acids of any of 56 transcription factor proteins CC appearing as ABO4303-ABO43148. Also included are altering the disease CC identifying a transformed plant (by: (a) transforming a plant with the recombinant polynucleotide, (b) selecting the transformed plants; and (c) cidentifying a transformed plant with an altered disease tolerance or resistance), altering the expression levels of at least one gene in a CC plant by transforming the plant with the recombinant polynucleotide, (b) comparing the plant with the polypeptide or polynucleotide cited above; (c) selecting a database sequence; (c) polynucleotide cited above; (c) selecting a database sequence; (c) polynucleotide cited above; (c) selecting a database sequence that meets caplynucleotide at low stringency with the polypeptide or comparising: (a) providing a plant to tast polynucleotide; (b) hybridising the selected colerance or treis; and (d) transforming the test polynucleotide in the plant) and altering a plant's trait (comprising: (a) providing a plant of the plant the recombinant polynucleotide contabase sequence in the plant) and altering a plant's trait (comprising: (a) providing the test polynucleotide in comparison to alter a trait of the plant. The transgenic plant is useful in comparison to alter a trait of the plant. The transgenic plant is useful in comparison to alter a trait of the plant. The transgenic plant is useful in comparison to alter a trait of the plant and plants with improved tolerance or resistance to pathogens and pests. The plants have commercial utility of resent the plant at transcription factor cDNA of the plants that is an Arabidopsis thaliana transcription factor cDNA of the plants thaliana transcription factor cDNA of the plants that is an arabidopsis thaliana transcription factor cDNA of the
                                                                                            Query Match
Best Local
                                                                          Matches
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Samaha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New transgenic plants comprising a recombinant gene that alters the plant's disease tolerance or resistance, useful in plant breeding, e.g. for generating plants with improved tolerance or resistance to diseases, pests or pathogens.
                                                                                                                                                    Sequence 2663 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 45-46; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BROU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2000; 2000US-00533029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2000; 2000US-00533029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ADAM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PINE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAMA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-521768/49.
                                                                        43;
                                  1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YU G.
RATCLIFFE
PILGRIM M.
JIANG C.
REUBER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEDDIE J.
PINEDA O.
ADAM L.
SAMAHA R.
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZHANG J.
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, Zhang J,
                                                                          Conservative
                                                                                                                                                  836 A; 544 C; 625 G;
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Yu G, Ratcliffe O, Pilgrim M, Jiang
                                                                                          78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic plant, comprising a recombinant
                                                                                            Score 40;
Pred. No.
                                                                          Mismatches
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                                                                                                                                                    658 T;
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Search completed: February 29, 2004, 20:36:03 Job time : 281 secs
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                                                                                                                                                                                        The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, flower senescence. Sequence information related to the polynucleotides flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                                Sequence 2663 BP; 836 A; 544 C; 625 G; 658 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 256; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                new plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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P-PSDB; ADD30228.
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Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEND-) MENDEL BIOTECHNOLOGY INC.
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seed germination rate; plant vigor; seedling vigor.
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                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 872)

Hunter.C. and Elgar.G.

Alpha2 adrenergic receptor gene
             Unpublished 2 (bases 1 to 872)
                                                                                                Horse alpha2 adrenergic receptor gene fragment probably genomic survey sequence.
AL606560
AL606560.1 GI:15591917
GSS; Alpha2 adrenergic receptor gene.
Equus caballus (horse)
Equis caballus (horse)
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Direct Submission

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2 (bases 1 to 1353)
2 (clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M. White,T.J., Sninsky,J.J., Direct Submission
Submitted (16.NOv-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1353)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Fodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M., White,T.J., Sninsky,J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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AY416856

Homo sapiens HCM6030 gene, VIRTUAL TRANSCRIPT, partial sequence, AY416856

AY416856

AY416856.1 GI:39772816
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113arity 100.0%; Score 51; DB 29; Length 1353; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                              library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 63 row: A column: 7
Seq primer: SP6 Class: BAC ends.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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Unpublished (1999)
Other_GSSs: RPCI-23-63A7.TV
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Centre Hinxton, Cambridge,
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12 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                  /lab host Fundamental Published Products were transformed into EcoRI sites. The ligation products were transformed into EcoRI sites.
                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10000"
/clone="RPCI-23-63A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Equus caballus"
|mol_type="genomic DNA"
                                                                                                                                                                                         /sex="Female"
                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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genomic clone
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; Murinae; Mus
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RESULT 5
BE097734/c
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AA943361/c
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ORGANISM
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Best Local
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Best Local :
            AUTHORS
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                                                                                                                                                                                                                                             403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvill
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                UI-R-BO1-aqb-a-11-0-UI.s1 UI-R-BO1 Rattus
UI-R-BO1-aqb-a-11-0-UI 3', mRNA sequence.
BE097734
                                                                                                                                                                                                                                                          1 GAGGATGAAGCTGAAGAGGAGGAAGAAGGAGGAGGAGGAGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
           1 (bases 1 to 517)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
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EST198860 Normalized rat brain,
 Normalization and
                                       Rattus.
                                                                                                                      BE097734.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Project:
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2012877"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: |
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           clone="RBRAI64"
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                                                                                                                      GI:8488660
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                                                                                                                                                                                                                                                                                                             81.6%;
91.7%;
            Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
 subtraction:
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Pred. No. 43;
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Pred. No. 43;
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                                                                  Euteleostomi;
                                                                                                                                                                           EST 12-JUN-2000
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                                                      Murinae;
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CF795982/c
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PUBMED
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Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Eukaryota; Metazoa; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 552)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
                                                                                                                                                                                                                                                                                  CF795982
892192 MARC 4PIG Sus scrofa cDNA 3', mRNA linear CF795982
CF795982.1 GI:37800555
                                                                                                                                                                                                                                                                                                     1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Dento-soares@ulowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first tail. The sequence tag present in the cDNA and therefore this may represent a bonafide poly A normalized corpus-striatum library cDNA Library Eroparation: M.B. Soares Lab Clone distribution: clones will be available through elements were found in this cDNA sequence: 365-436,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coordinated Laboratory for Computational Genomics University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 5224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                               / October 1141= 114 - N-DOLI.
/ October Vector: pi7773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI. The library of the following tissues: thalamus, cereballum, corpus striatum and hippocampus. For a detailed derived, please visit only from which this clone was ratest.eng.uiowa.edu. The subtraction has been previously corpus of the library from which this clone was described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=corpus-striatum
TAG_LIB=UI-R-BO1
                                                                                                                                                                                                                                                                                                                                                                                                                                      "AG_SEQ=CTAGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="sprague-Dawley"
/Ab xref="taxon:10116"
/clone="UI-R-BO1-aqb-a-11-0-UI"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/mol_type="mRNA"
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lone_lib="UI-R-BO1"
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91.7%;
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Pred. No. 44;
0; Mismatches
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AJ517718/c
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rocus

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Similarity
                                                                                                                                                                                                   Laboratory of Ecotoxicology
University of Le Havre
25 rue P. Lebon, 76058 Le Havre CEDEX, France.
Location/Qualifiers
                                                                                                                                                                                                                                                                  Contact: Danger J-M
                                                                                                                                                                                                                                                                                                                    Dreissena polymorpha
Dreissena polymorpha
Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Dreissenoidea; Dreissenidae; Dreissena.
                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                            Dreissena polymorpha
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 604)
Bultelle,F., Panchout,M., Leb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 GAGGATGAAGATGAAGAGGAGGACGAGGACGAGGAGGATGAAGAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                      AJ517718

AJ517718 Dreissena polymorpha
chron35, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          AJ517718.1 GI:25778429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
Plate: TWW8018 row: D column. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                   /organism="Dreissena polymorpha"
|mol_type="mRNA"
|db_xref="taxon:45954"
|clone="chron35"
|clone_lib="Dreissena polymorpha mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol_type="mRNA"
/db xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DHIOB"
                                                                             81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 row: D column: 17
                                                          Score 41.6; DE
Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.6; pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                            604 bp |
orpha mRNA
                                                                                                                                                                                                                                                                                     Leboulenger,F. and Danger,J.-M.
                                                                                _ DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear EST
Dreissena polymorpha
                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
                                                                             Length 604;
                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 552;
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Tha cDNA clone
                                                Gaps
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RESULT 9
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ORGANISM
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                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                        101
pgfin.pk007.124 normalized chicken fat cDNA linear EST 15-JUN-2001 cDNA clone pgfin.pk007.124 5' similar to gi|4506411 ref|NP 002874.1| Ran GTPase activating protein 1; Fugl [Homo sapiens] gi|11418178 ref|XP 010014.1| Ran GTPase activating protein 1 [Homo sapiens] sp|P46060|RGP1_HUMAN RAN-GTPASE ACTIVATING PROTEIN 1 pir|138146 RanGAP1 - human pir|JC, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
Gpieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 102 row: K column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCI-23-102K10.TV RPCI-23 Mus musculus genomic clone RPCI-23-102K10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other GSSs: RPCI-23-102K10.TJ
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ288043
AZ288043.1 GI:9529829
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mue musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nierman, W., Feldblyum, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRI Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="RPCI-23-102K10"
                                                                                                                                                                                                                                                                                                                                                                                                  81.6%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                               Score 41.6; DI
Pred. No. 46;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            713;
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REFERENCE
AUTHORS
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ORGANISM
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AUTHORS
TITLE
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SOURCE
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Focus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 4 row: L column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                 Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH309086 668 bp DNA linear GSS 03-DEC-20
CH230-4L16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGA
                                                                                                                                                                                                                                                                                                  Riggs,F., de Jong,P. and Fraser,c.m.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                        Zhao,S., Shetty,J., Shatsman,S., Tse
Shvartsbeyn,A., Gebregeorgis,E., Ove
Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Delaware
Townsend Hall, Newark, DE 19717, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cogburn, L.A., Morgan, R.W. and Chicken ESTs from fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI067787.1
                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH309086.1 GI:17234555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH230-4L16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
row: L
er: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgf1n.pk007.124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="fat"
/lab host="E.coli EMDH10B"
/clone lib="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .640
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                                                                                                                                                                                                                                                                                                                                                Tsegaye, G., Overton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG
                                                                                                                                                                                                               MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 640;
                                                                                                                                                                                                                                                                                                                                                Geer, K.,
Russell, D.,
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
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Class:

BAC ends

0

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Query Match
Best Local Similarity 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Phasianinae; Gallius.

1 (bases 1 to 723)

Boardman, P. B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Frong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU121352.1 GI:25331126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU121352 723 bp n
603146064F1 CSEQCHL17 Gallus gallus
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118
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//olone lib="CSBCHL18"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                       /strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST145016"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="BN/S8NHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-4L16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
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91.5%;
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Pred. No. 71;
0; Mismatches
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CDNA clone ChEST145016 5', mRNA
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                                                       ACCESSION
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AQ875889
LOCUS
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Best Local S
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AUTHORS
TITLE
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SOURCE
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DEFINITION
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BE613618
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                                                                             AQ875889
V130F6 mTn-3xHA/lacZ Insertion cerevisiae genomic 5', genomic
Saccharomyces cerevisiae Saccharomyces cerevisiae
                                                          Cerevisiae
AQ875889
AQ875889.1
GSS.
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                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Library Linl.gov
Plate: LLDAM9714 row: 1 column: 02
High quality sequence stop: 711.
Location/Qualifiers
                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 753)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE613618
601504406F1 NIH MGC 71 Homo sapiens
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43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          /Organism="Homo sapiens"
/organism="Homo sapiens"
/mb type="mkNA"
/db xref="taxon:9606"
/clone="IMAGE:3966193"
/tissue type="lelomyssarcoma"
/lab host="PH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned uniddirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                 GI:6288133
                                                                                                                                                                                                                                                                                                                                                                            79.6%;
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[5' aattctttttttcggatccggggctgcacgc] "
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91.5%;
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            (baker's yeast)
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n Library, strain y
c survey sequence.
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8 Saccharomyces
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FEATURES

source

COMMENT

TITLE
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AUTHORS

VERSION KEYWORDS

ACCESSION

DEFINITION

SOURCE

ORGANISM

RESULT 11 BU121352

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ORIGIN

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260
                                      RAT BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                  Riggs, F.,
Rat BAC E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                     Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                            GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            CH230-400D22, genomic survey sequence.
BZ227940
BZ227940.1 GI:23886481
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CH230-400D22.TJ CHORI-230 Segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te of mTn-3xHA/lacz insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yale University
P.O. Box 208103, New Haven,
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kumar A
Michael Snyder, Dept.
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Email: szhao@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anuj.kumar@yale.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="mTn-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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/mol_type="genomic_DNA"
/strain="Y2278 - S288C_background, cir(0) rho(0)"
/db_xref="taxon:4932"
/lab_host="E._coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.6;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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  rat BAC library CHORI-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 400 row: D column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Plate: LLAM13316 row: m column:
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Class: BAC ends.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 703.
Location/Qualifiers
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                                   /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo.
Average insert size 2 kb. 
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Brain"
/clone_lib="CHRI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
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/strain="BN/S8NHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-400D22"
                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                         clone="IMAGE:6055864"
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91.5%;
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Pred. No. 73;
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BM807097
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Best Local (
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                                                                                     BB852469 RIKEN full-length enriched, B16 F10Y cells cDNA clone G370007K15 5', mRNA sequence.
                            Mus musculus
                                  Mus musculus (house mouse)
                                                            EST
                                                                  BB852469.1 GI:17093923
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Plate: LLAM12266 row: 1 column: 23
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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BM807097
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AGENCOURT 6552940 NIH MGC 85 Homo Bapiens cDNA clone
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43; Conserv
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                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                            /tissue_type="lymphoma, cell line"
//ab_host="DH10B (phage resistant)"
/clone_lib="NIH_MCC_85"
/note="organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size_1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MCC_Library."
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:5552038"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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91.5%;
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Pred. No. 78;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
(11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
further details.
e mouse tissues.
                                                                                                                                                                                                                                                                                                75
Mus musculus
Mus musculus
                                                                                                BX519271 Sugano mouse kidney mkia Mus musculus IMAGD998J204714 ; IMAGE:1922035, mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akinura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saitto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaski, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
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1. (bases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370007K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism≈"Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                      GI:32295277
                  (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        79.2%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                              Score 40.4; D
Pred. No. 74;
0; Mismatches
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AZ208950
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Fax: +49 30 32639 111
                                Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoida;
                                                                                                                                                                     AZZ08950
786 bp DNA linear GSS 31-AUG SP 0138 AZ C06 T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratu genomic clone Plate=138 Col=12 Row=E, genomic survey sequence.
AZZ08950
                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further inform sugF, Primer sequence: CTTCTGCTCTAAAAGCTGCG.

Location/Qualifiers
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RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
                                                                                                                                AZ208950.1 GI:8422136 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Ina Rolfs
                Strongylocentrotidae; Strongylocentrotus
                                                                                                    Strongylocentrotus purpuratus
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_ib="Sigano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCC and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/mol_type="mRNA"
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/lab_host="DH10B"
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/clone="IMAGp998J204714 ;
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Pred. No. 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
                                                                                                                                                                                                                                        Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (199)
Other_GSSs: CH230-504N18.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                         9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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Location/Qualifiers
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Class: BAC ends
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California Institute of Technology
Pasadena California 91125, USA
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                                                                                                                                                                                                                            Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ152227.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cameron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:7668"
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Lehrach,H., Britten,R.J, Davidson,E.H.
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Overton,L., Russell,D., Chen,D.,
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FEATURES

Seq primer: SP6 Class: BAC end-

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Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
Plate: 447 row: L column: 4
                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riggs, F., de Jong, P. and Fraser, C.M. Russell, D., Rat BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Shetty,J., Shatsman,S., Taegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH230-447L4. TJ CHORI-230 Segment 2 Re
CH230-447L4, Genomic survey sequence.
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Plate: 504 row: N column: 18
                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic_DNA"
/strain="BN/S8NHsd/MCW"
/db_xref="taxon:10116"
                                       /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI,
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
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/strain="BN/SsNHsd/MCW"
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| mol_type="genomic norvegicus"
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Pred. No. 80;
0; Mismatches
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Russell, D., Chen, D.,
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S Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Lev Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)
Other GSSs: RPCI-24-401L13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
712 Medical Center Dr., Rockville, MD 20850, USA
                   1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAAGAG 48
                                                                                          43;
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong Resources (http://www.chori.org/bacpac/pacferingframe.htm). BAC plate: 401 row. tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Seq primer: SP6 Class: BAC ends.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RPCI-24-401L13.TJ RPCI-24 Mus musculus genomic clone
PCI-24-401L13, genomic survey sequence.
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                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Gell type="Spleen/Brain"
/Gell type="Spleen/Brain"
/Glone lib="RPCI-24"
/Glone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-24-401L13"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .152
                                                                                            78.4%;
89.6%;
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88.0%;
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Pred. No. 78;
0; Mismatches
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Pred. No. 80;
0; Mismatches
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 67
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FEATURES

Class: BAC ends.

Location/Qualifiers

1. .834

source

/sex="Female" /cell type="A

0,

Gaps

0,

/clone="CH230-447L4"

COMMENT

TITLE JOURNAL

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

BZ249816.1 GI:23911056

ORGANISM

ACCESSION DEFINITION RESULT 21 BZ249816

밁 S

ORIGIN

'sex="Female"

Matches Query Match

44; Similarity

Conservative

٥,

GSS 19-JUL-2001

Gaps

0,

79.2%; 88.0%;

Local

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RESULT 24
CA315228/c
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Best Local :
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                                                                          256 bp
UI-M.FW0-cbi-b-15-0-UI.rl NIH BN
IMAGE:6809872 5', mRNA sequence.
CA315228
CA315228.1 GI:24533352
EST.
                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC (page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 257 row: L column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-24-257L19.TJ
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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BH072396.1 GI:14891993
GSS.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 167)
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RPCI-24-257L19.TV RPCI-24 Mus mu
                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Spleen/Brain"
/clone_lib="APCI-24"
/clone_lib="APCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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/sex="Male"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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89.6%;
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                                                                                                                                                           musculus
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AUTHORS
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SOURCE
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CF897938/c
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 330)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                             CF897938 330 bp
A0231H07-5 NIA Mouse Embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAGAG 48
                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                  CF897938.1 GI:38164987
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
CF897938
                                                                                                                                                                                                                                                                                                                                                                                                           subtracted)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The following repetitive elements were found in this cDNA sequence: 37-156, >(GGA)n#Simple repeat (matched compliment) 82-200, >(GAA)n#Simple repeat (matched compliment) 201-254, > (GGA)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FWO"
/clone_lib="NIH BMAP]
/clone_lib="NIH BCOR_IIB="NIH BMAP]
/clone_lib="NIH BCOR_IIB="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP]
/clone_lib="NIH BMAP_lib="NIH BMAP_li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    program coordinator."
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/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:6809872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .256
                                                                                                                                                                                                                                                                                                                                                                                                           330 bp mRNA linear EST 04-NOV-2003
NIA Mouse Embryonic Germ Cell cDNA Library (Long,
Mus musculus cDNA clone NIA:A0231H07 IMAGE:30731418 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.4%;
89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
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           cDNA libraries from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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4.
                                                                                                                    Euteleostomi; 
murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 04-NOV-2003
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DEFINITION
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LOCUS
                                                                                                                                             RESULT 26
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Best Local (
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MEDLINE
PUBMED
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                                                                                                                                                                                              325
                                             AL135731
331 bp mRNA linear
DKFZp434H0531_r1 434 (synonym: htes3) Homo sapiens
                                                                                                                                                                                        Similarity 89.6
43; Conservative
                                                                                                                                                               Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0231 row: H column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6 (Invitrogen); Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural This is a long-transcript enriched cDNA library (Ref. cells were obtained from Dr. Brigid L.M. Hogan and RNA were cultured at 37. C, 5% CO2 in DMEM supplemented with acids, 2 mM glutamine, penicillin/streptomycin, 1 mm units of LIF per liter. Double-stranded CDNA library from Synthesized with an Oligo (dT) primer [Invitrogen: 2.5 up of total RNA, treated with To Long-linker LJ-Sall, purified by phenol/chloroform, and to Long-linker LJ-Sall, purified by phenol/chloroform, and to Long-linker LJ-Sall, purified by phenol/chloroform, and cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sall-S. The then purified by phenol/chloroform and converse out to were double digested with a primer Sall-S. The then purified by phenol/chloroform and Centricon 100. Then, the procedure by Dr. Kazuhiro Kondo at AISIN Cosmos. Then the cDNAs were cloned with The Ligation method. The procedure by Dr. Kazuhiro Kondo at AISIN cosmos. Then the community was constructed by Yulan Piao and Kazuhiro Kondo. The library was constructed by Yulan Piao and Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 330
                                                                                                                                                                                                                                                                           78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library
[Long, subtracted]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="embryonic day 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="NIA:A0231H07 IMAGE:30731418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57Bl6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="niaEST:A0231H07-5"
xref="taxon:10090"
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                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                               Length 330;
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                                                 EST 04-SEP-2003
CDNA clone
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                                                                                                                                                                                                                                    Gaps
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AUTHORS
TITLE
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VERSION
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ORGANISM
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CD564037/c
                                                                                                                                               JOURNAL
MEDLINE
PUBMED
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Best Local Similarity
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AUTHORS
TITLE
JOURNAL
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VERSION
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SOURCE
ORGANISM
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Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: B0473 row: A column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 to 358)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplificati;
                                                                                                                                             11544199
                                                                                                                                                                          Genome Res. 11
                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                        80473A03-5 NIA MOUSE E6.5 Whole E musculus cDNA Clone NIA:B0473A03 CD564037 GI:31607930 EST.
                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No s1 sequence available.
This clone (DKRZp434H0531) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum,H., Bauersachs,S., Mewes,W., Weil,B. and Wiemann,S. EST (Blum,H., Bauersachs,S., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL135731.1 GI:6603918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="maRNA"
/db xref="maxNc:9606"
/clone="DKFZp434H0531"
/tisuue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'dev_stage="adul1"
'dev_stage="adul1"
'lab_host="0H10B"
'lab_host="0H10B"
'clone lib="434 (synonym: htee3)"
'note="Vector: pSportl; Site_1: NotI; Site_2:
                                                                                                                                                         (9), 1553-1558 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.4%;
89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 mRNA linear
Embryo cDNA Library
3 IMAGE:30445634 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
                                                                                                                                                                                  PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                              EST 11-JUN-2003 (Long) Mus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 365)

Okazakl, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D., P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Flatcher, C.P., Porrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
                                                                                                                                                                                                                                                                                                                                                                   BY054209 alKEN full-length enriched, clone 1730076P21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                    BY054209.1 GI:26159657
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                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 7 embryos at 6.5-days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at 6.5-days postcoitum'
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NIA Mouse E6.5 whole Embryo cDNA Library
(Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="NIA:B0473A03 IMAGE:30445634"
/tissue_type="E6.5 whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C578L/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _type="mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stage="whole embryo including extraembryonic tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
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87;
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d, TIB-55 BB88 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIXEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues
Please visit our web
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="traxon:10090"
/clone="I730076P21"
/cell_line="TIB-55 BB88"
/clone_lib="RIKEN full-length enriched, TIB-55
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                                                                                                                                                          78.4%;
89.6%;
                                                                                                                     0,
                                                                                                                                                              Score 40;
Pred. No.
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                                                                 Email: genome-res@go.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H.,
Myazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Computational Analysis of Full-Length Mouse cDNAs Compared with
Hyashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Normalization and subtraction of cap-trapper-selected cDNAs to
genes. Genome Res 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
10 (11), 1757-1771 (2000)
Commutar-based methods for the control of cap-trapper sequencer. Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusto, V., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusto, V., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T.A., Gustinoldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gastinoldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gastinoldi, M., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, M.J., Pertea, G., Pesole, G., Martinoldi, A., Schneider, C., Semple, C.A., Setou, M., Sindada, K., Verardo, R., Wagner, L., Walker, M.S., Taskanaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varadio, T., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Varadio, T., Wanner, M.S., Shinada, K., Wallana, R., Takenaka, T., Teasdale, R.D., Tomita, M., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Sakazume, N., Salo, K., Hara, A., Hashizume, M., Toxawa, K., Yang, L., Yuan, Z., Zavolan, M., Yang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Yan, Y., Zimmer, A., Carninci, P., Sakazume, N., Yang, I., Misaki, K., Kawai, J., Aizawa, K., Yang, J., Yuang, J., Yuang, J., Wallana, R., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Ishi, Y., Shinaga, S., Hara, A., Hashizume, M., Imotani, K., Ishi, Y., Shinaga, J., Wallana, J., Yang, J., Jaka, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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(bases 1 to 365)
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for the mouse full-length cDNA sequence clustering for construction of
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Sciurognathi; Muridae; Murinae; Mus.
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Matches 43
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                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: Cdna@lgsun.grc.nia.nih.gov Plate: CO264 row: C column: 01 Seg primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Other_ESTs: C0264C01-3
                                                                                                                                                                                                                                      OLYA=No.
                                                                                                                                                                                                                                                                                                                                                                   Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Systematic Analyses
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Luo,A. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CO264C01-SN NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus cDNA clone NIA:CO264C01 IMAGE:30016728 5', mRNA sequence. CA538239 CA538239.1 GI:25079717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology/Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                             quality sequence stop: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
/tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
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                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="bone marrow"/cell_type="macrophage"
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/mol type="mRNA"
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89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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Pred. No. 87;
0; Mismatches
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87;
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                            0;
                            Gaps
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Search completed: February 29, 2004, 21:48:03 Job time : 2176 secs

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Matches

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1181, Application US/09016434
PREENT NO. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALLFORNIA
CONTINENT. TO SONIA
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               COMPUTER READABLE FORM:
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                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Thang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Yi, Guo-Liang
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-Olo
CURRENT APPLICATION NUMBER: US/09/533,029
FERLIER APPLICATION NUMBER: 60/125,814
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN PATE: 1999-03-23
SOFTWARE: PATENTIN Ver. 2.1
; OTHER INFORMATION: G1089 US-09-533-029-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE;
; LIBRARY: GENBANK
; CLONE: G178197
US-09-016-434-1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4'
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
APPLICATION:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) B45-4166
                                       LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-533-029-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47, Application US/09533029
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ilarity 100.0%; Pred. No. 2.8e-05;
Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1668
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-736-457-1668
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Best Local Similarity 87.5
Matches 42; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1668
LENGTH: 636

TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                         APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   865 GATGACGAAGATGAGGAGGAGGAAGAGAGGAGGAAGAGGAGGAAGAG 912
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Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                             Vedvick, Tom
Carter, Darrick
                                                                                                                                                                                                                              Mannion, Jane
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Lodes, Michael A.
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Lodes, Michael A.
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Bangur, Chaitanya S.
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89.6%;
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87.5%;
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Pred. No. 0.019;
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                                              ; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1668
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                                                                                                            SOFTWARE: Fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.3%;
Best Local Similarity 87.5%;
Matches 42; Conservative
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Best Local (
Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
NUMBER OF SEQ ID NOS: 1668
                                                                                                                                       APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478612
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
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ORGANISM: Homo sapiens
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Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                             FastSEQ for Windows Version 3.0
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Vedvick, Tom
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Lodes, Michael
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Retter, Marc
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r, Chaitanya
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87.5%;
75.3%;
87.5%;
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Score 38.4; DB Pred. No. 0.045;
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               4.
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Matches

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US-09-220-132-31

Sequence 31, Applicati
Patent No. 6506607

GENERAL INFORMATION:
APPLICANT: Shylan, F
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APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 650
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NAME/KEY: misc_feature

LOCATION: (1) - (650)

OTHER INFORMATION: n = A,T,C or G

US-09-328-111-333
                                                                                                                                   SOFTWARE: 1
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                    APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT

TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE

FILE REFERENCE: 07344-074001

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT FILING DATE: 1998-12-23
                                                                                                                                              NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.3%;
Best Local Similarity 87.5%;
Matches 42; Conservative
                                                     LENGTH: 1194
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. 62022
Paten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-328-111-333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48
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                          RESULT 10
US-08-860-038-16/c
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                                                                                                                                                                                                                                                                                                                            ; STRANDEDNESS: BINGle
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-15
             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                         Matches
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Best Local (
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US-08-860-038-15
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR9
ATTORNEY/AGENT INFORMATION:
NAME: CASSIFIC STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Applicat Patent No. 6287762 GENERAL INFORMATION:
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Best Local (
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TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPMADE: PS-TEN-T-T-DOS
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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16, Application US/08860038
                                                                                                                                           635 GÁGGÁGGÁAGGTGÁGGÁAGÁTGÁAGÁGGÁTGÁGGÁGGÁGGÁGGÁAGÁ 681
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6287762
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Similarity 87.2%;
41; Conservative
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ilarity 85.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (610) 454-3816
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                                                                                                                                                                                                                                         Score 36.8; DB 3; Pred. No. 0.099;
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Patent No. 6287762

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US-09-580-923-15
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REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEPHONE: (610) 454-3808
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                            Patent No.
APPLICANT: Wils, Pièrre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURLFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804.0138-01
CURRENT FILING DATE: 0200-05-26
PRIOR APPLICATION NUMBER: 08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
PILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/01468
PILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11: MOLECULE TYPE: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 500 Arcola Road, Mailstop 3C43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
/desc = "Oligonucleotide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.8; DB : Pred. No. 0.099;
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                                                                                                                                                                              RESULT 13
US-09-894-998A-34/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: POSEQ ID NO 16
LENGTH: 58
TYPE: DNA
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LENGTH: 58
                                                                                                                          Sequence 34, Application US/09894998A Patent No. 6537555
GENERAL INFORMATION:
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Best Local &
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Best Local (
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APPLICANT: Blanche, Francis

TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH TITLE OF INVENTION: IMMOBILIZED OLIGONUCLECTIDE

FILE REFERENCE: 03804.0138-01

CURRENT APPLICATION NUMBER: US/09/580,923

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 08/860,038

PRIOR FILING DATE: 1997-06-09

PRIOR APPLICATION NUMBER: PCT/FR95/01468

PRIOR APPLICATION NUMBER: PCT/FR95/01468

PRIOR APPLICATION NUMBER: 995-11-08

NUMBER OF SEQ ID NOS: 36

NUMBER OF SEQ ID NOS: 36
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APPLICANT:
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                                                                      APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
                                                       APPLICANT:
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                                        APPLICANT:
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                        Sleath,
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Wils, Pierre
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                                                       McGowan, Patrick
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Paul R.
COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 36.8; DB 85.4%; Pred. No. 0.099;
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US-09-163-285-3
                                                   Query Match
Best Local S
Matches 41
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                                                                                                                                                                                                  TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/09/163,285
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
                                                                                                                                   FEATURE
                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local S
                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION.
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 210121.538
CURRENT FILING DATE: US/09/894,998A
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 661
                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/0
FILING DATE: June 24, 19
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
60/090,398
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                                                                                                                                                 STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02109
ADDRESSEE:
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3, 620401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
                                               Conservative
                                                                                                        CDS
1..744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 State Street
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                                                                                                                                                            single
                                                        72.28;
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                                       Score 36.8; DE
Pred. No. 0.12,
0; Mismatches
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                                                  DB 3;
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                                                        Length 744;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                  0;
                               Gaps
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RESULT 16
US-09-702-705-316
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                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-163-285-1
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Best Local S
                                                                                                                                       Sequence
                                                                                                                           Patent No.
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION UNMBER: 60/090,39;
APPLICATION NUMBER: 60/090,39;
FILLING DATE: JUNE 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-163-285-1
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application Patent No. 6204013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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CORRESPONDENCE ADDRESS:
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                                                                                                          INFORMATION:
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                                                                                                                                  316,
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                                                                                                                           6504
         Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
                                                               WANTION:
Wang, Tongtong
Wang, Chaitanya S
""" And A.
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Fan, Liqun
                                                                 Bangur, Chaitar
Lodes, Michael
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28 State Street
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TENTION: NOVEL MSP-
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85.4%;
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24, 1998
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CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FRACESEQ for Windows Version 3.0
SEQ ID NO 316
SEQ ID NO 316
LENGTH: 1633
TYPE: DNA
RCANISM: Homo sapiens
US-09-702-705-316
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US-09-736-457-316
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US-09-702-705-788
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US-09-702-705-788
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SEQ ID NO 788
LENGTH: 1633
TYPE: DNA
                                                                                                                                        Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                          Sequence 316, Application US/09736457 Patent No. 6509448
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.2%;
Best Local Similarity 85.4%;
Matches 41; Conservative
                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                         Matches
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
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                                             APPLICANT
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                788, Application US/09702705
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l Similarity 85.4%;
41; Conservative
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Wang, Tongtong
Chaitanya S
                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
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Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Bangur, Chaitanya S.
Lodes, Michael A.
Fan, Liqun
Wang, Aijun
                                                       Fanger, Gary
Vedvick, Tom
Carter, Darrick
                            Retter, Marc
Mannion, Jane
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                                                                                                                                                                                                                                                                                                                   Score 36.8; DB Pred. No. 0.12;
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; SOPTWARE: FastSEQ for Wi
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-316
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US-09-736-457-788
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SEQ ID NO 788
LENGTH: 1633
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Best Local Similarity 85.-
41; Conservative
                                                                                                                                                                  Sequence 316, Application US/09614124B Patent No. 6630574
                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity 85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
NUMBER OF SEQ ID NOS: 1864
NUMBER OF SEQ ID NOS: 1864
                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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                                     APPLICANT:
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                       APPLICANT:
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: Mannion, Jane
INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
                                   Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Vedvick, Tom
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Lodes, Michael A.
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Retter, Marc
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; TYPE: DNA ; ORGANISM: Homo sapiens US-09-614-124B-316

Query Match Best Local (

CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 316
LENGTH: 1633

TITLE OF INVENTION: DIAGNOS FILE REFERENCE: 210121.478C9

DIAGNOSIS OF LUNG CANCER

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APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Darrick
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121, 478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FASSISEQ for Windows Version 3.0
LENGTH. 1638
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; ORGANISM: Homo sapiens
US-09-614-124B-788
                                                                                                                                                         GENERAL INFORMATION:
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US-09-614-124B-788
                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                            Local Similarity 85.4
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                                                                                                                                                                                                                                   INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND INVENTION: DIAGNOSIS OF LUNG CANCER SEENCE: 210121.478C12
                                                                                                                                                                      316, Application US/09671325
5. 6667154
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                                                   Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Lodes, Michael
                                                                                                        Fanger, Gary
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,, Tongtong
ur, Chaitanya g
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                                          Liqun
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85.4%;
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                                                                                                                                                                                                                                                                                                   Score 36.8; DB 4;
Pred. No. 0.12;
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Pred. No. 0.12;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                            Length 1633;
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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
FILE REFERENCE: 210121,478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 788
LENGTH: 1633
TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-788
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                                                                                                                                                                                                                                         US-09-589-184-316
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SEQ ID NO 316
LENGTH: 1633
TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-316
            APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121,478C8
FILE REFERENCE: 210121,478C8
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US-09-671-325-788
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Best Local Similarity 85.4%;
Matches 41; Conservative
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                                                                                                                                                                                                                Patent No.
   CURRENT FILING DATE:
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Best Local s
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CURRENT FILING DATE: 2000-09-26
                                                                                                                                                                                         INFORMATION:
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Lodes, Michael
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, Tongtong
mir, Chaitanya g
MBER: US/09/589,184
2000-06-05
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Pred. No. 0.12;
0; Mismatches
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Pred. No. 0.12;
0; Mismatches
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; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-589-184-316
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; ORGANISM: Homo sapiens
US-09-589-184-788
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SEQ ID NO 788
LENGTH: 1633
                                                                                                                                                                                                                                                            Sequence
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Best Local Similarity 85.4%;
Matches 41; Conservative
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Best Local Similarity
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 210121.478C8
CURRENT APPLICATION NUMBER: US/0;
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
                                                                                                                                                                          APPLICANT:
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Zhang, Jie
Ren, Felyan
Chen, Rui-hong
T: Zhao, Qing A.
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Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                    Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Lodes, Michael A.
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di, Vinod
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85.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 1633;
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 7984C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL genes Version 1.0
SEQ ID NO 1085
LENGTH: 2817
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHES, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULAT
FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 5561
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                                                                                             RESULT 28
US-09-418-710-30
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.4
Conservative
GENERAL INFORMATION:
APPLICANT: Jones, N
TITLE OF INVENTION:
                                                     Sequence 30, Appli
Patent No. 6596482
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOGATION: (346)...(4926)
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Patent No. 6596482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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LOCATION: (109)..(2817)
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                                                                                                                                                                             4123 GATGAAGAGGAGGAAGAAGAAGAGGAGGAGGAAGAAGATTAT 4170
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                                                                           Application US/09418710
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nilarity 85.4%;
Conservative
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Michael

TRANSCRIPTIONAL REGULATOR

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Sequence 12, Application US/09356952
Patent No. 611763
GENERAL INFORMATION:
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER APPLICATION NUMBER: 60/093,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6114
TYPE: DNA
ORGANISM: Mus musculus
US-09-495-714C-5
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US-09-356-952-12
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US-09-495-714C-5
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Query Match
12.2%; Score 36.8; DB 4; Length 6114;
Best Local Similarity 85.4%; Pred. No. 0.14,
Matches 41; Conservative 0; Mismatches 7; Indels 0
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LOCATION: (346)...(4938)
US-09-418-710-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University Technologies International Inc.
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) IF-SUBUNIT GENE
FILE REFERENCE: 45499.4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.2%;
Best Local Similarity 85.4%;
Matches 41; Conservative
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CURRENT APPLICATION NUMBER: US/09/418,710
PRIOR APPLICATION NUMBER: DCT/UF98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
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                                                                                                                                                                                                                                                                                                                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAG 48
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Listing first 150 summaries
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1: //ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: //ggn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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4: //ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

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11: //ggn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: //ggn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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18: //ggn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

18: //ggn2_6/ptodata/2/pubpna/US09_PUB.seq:*

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      2353733 seqs, 1803733377 residues
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14 US-10-001-073-1
15 US-10-305-720-1181
15 US-10-255-567A-41
16 US-09-972-5466-16
17 US-09-972-546-16
18 US-09-728-444-146
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Sequence 31, Appl
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Sequence 28, Appl
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Sequence 20, Appl
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19 US-09-864-761-286

14 US-10-29-366-4712

3 14 US-10-29-366-4712

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3 15 US-10-101-487-76

5 14 US-10-29-386-20317

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15 US-10-424-599-44115

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6 14 US-10-29-4749-1309

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2 14 US-10-027-336-234-3

3 15 US-10-027-33-2-324-3

6 10 US-09-864-761-4816

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1 US-10-027-33-2-325-3

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9 US-09-925-300-817
15 US-10-242-535A-22486
9 US-09-864-761-2913
14 US-10-116-712-178
15 US-10-242-535A-26235
                                                                                                          ALIGNMENTS
                                                                                                                                                                                                 Sequence 287, Applesquence 4171, Applesquence 4171, Applesquence 4171, Applesquence 4171, Applesquence 76, Applesquence 76, Applesquence 76, Applesquence 62, Applesquence 53, Applesquence 62, Applesquence 62, Applesquence 62, Applesquence 62, Applesquence 1714, Applesquence 1715, Applesquence 1717, Applesquence 64, Applesquence 15, Applesquence 16, Applesquence 16, Applesquence 17, Applesquence 2152, Applesquence 237, Applesquence 238, Applesquence 337, Applesquence 238, Applesquen
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                                                                                                                                               US-10-077-870-3

Sequence 3, Application US/10077870

Publication No. US2030003470A1

GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
ITILE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
CURRENT APPLICATION NUMBER: US/10/077,870

PRIOR APPLICATION UNUMBER: US/10/077,870

PRIOR PILING DATE: 2002-05-21

PRIOR PILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 3

LENGTH: 1353

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Marku
APPLICANT: Koulu, Marku
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Lakka, Timo A
APPLICANT: Nomainen, Tomi-Pekka
APPLICANT: Namarinen, Kristina
APPLICANT: Salonen, Kitta
APPLICANT: Valkonen, Ritta
APPLICANT: Valkonen, Nitsi
APPLICANT: Valkonen, Nitsi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: Protein, and uses thereof
CUREEN FILLING DATE: 2000-04-05
PRIOR FILLING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US/09/825,923
PRIOR APPLICATION UMBER: US
                                     FEATURE:
| PEATURE: CDS | NAME/KEY: GDS | NAME/KEY: GDS | LOCATION: (1)...(1350) | OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor US-10-077-870-3
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Matches 51
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Conservative 0; Mismatches 0; Indels
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RESULT 1
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'Sequence 3, Application US/09825923
'Patent No. US20010016338A1
'GENERAL INFORMATION:
'APPLICANT: Snapir, Amir
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Score 51; DB 14; Length 13 Pred. No. 9.7e-06; Mismatches 0; Indels

Length 1353;

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Gaps

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Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
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Publication No. US20030113725A1

GENERAL INFORMATION:

APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION UNMBER: US/10/001,073

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
LENGTH: 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
CURRENT FILING DATE: 2002-11-26
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
                                                             APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/016,434 PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature OTHER INFORMATION: Genbank ID No. US20040010136A1 g178197
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Pred. No. 9.7e-06;
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                                                                                                                                                                                                                                            Sequence 16, Application US/09972546 Publication No. US20030124704A1 GENERAL INFORMATION:
SEQ ID NO 16
LENGTH: 215980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: F
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/10034650 Publication No. US20030216558A1 GENERAL INFORMATION:
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LENGTH: 3274
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                                                                                                                                                                    APPLICANT: CATE, RICHARD L.
APPLICANT: SAH, DINAH W.Y.
TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/034,650 CURRENT FILING DATE: 2002-07-23 PRIOR APPLICATION NUMBER: US 09/474,377 PRIOR FILING DATE: 1999-12-29 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02
                                                                                                            FILE REFERENCE: A116US
CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT FILING DATE: 2001-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                          PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                           APPLICANT: STRITTMATTER, STEPHEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Morris, David APPLICANT: Engelhard, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
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                                      SOFTWARE: PatentIn Ver.
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100.0%; Pred. No.
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Pred. No. 0.0037;
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TYPE: DNA

ORGANISM: Mus

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COCATION: (102) (1325) (1327)

NAME/KEY: modified base
OTHER INFORMATION: (2027)
NAME/KEY: modified base
OTHER INFORMATION: a, t, C, 9, other or unknown
LOCATION: (1728) (1728) (1728)

NAME/KEY: modified base
OTHER INFORMATION: a, t, C, 9, other or unknown
LOCATION: (1728) (1728) (1728)
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NAME/KEY: modified base
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OTHER INFORMATION: a, t, C, 9, oth
LOCATION: (93794) base
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LOCATION: (96570). [96573)
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LOCATION: (96570). [96573)
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LOCATION: (96715). (96814)
OTHER INFORMATION: a, t, C, 9, oth
LOCATION: (104447). (104546)
OTHER INFORMATION: a, t, C, 9, oth
LOCATION: (104447). (104546)
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LOCATION: (104546)
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LOCATION: (104546) NAME/KEY: modified\_base
LOCATION: (51380)...(51479)
NAME/KEY: modified\_base
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NAME/KEY: modified\_base
LOCATION: (56740)
NAME/KEY: modified\_base
LOCATION: (56740)
NAME/KEY: modified\_base
LOCATION: (56765)...(56644)
NAME/KEY: modified\_base
LOCATION: (5765)...(56644)
NAME/KEY: modified\_base
LOCATION: (57818)...(62917)
NAME/KEY: modified\_base
LOCATION: (58518)...(62917)
NAME/KEY: modified\_base
LOCATION: (68518)
NAME/KEY: modified\_base
LOCATION: (68534)...(68633)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (68534)...(68633)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (74552)...(74651)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (74552)...(74651)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (81446)...(81454)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (81446)...(81451)
OTHER INFORMATION: a, t, c, g, other or unknown
LOCATION: (88519)...(88618)
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LOCATION: (88519)...(88518)
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LOCATION: (88519)...(88518)
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LOCATION: (88519)...(88518) COCATION: (114521) THER INFORMATION: a, t, ç á g, other or unknown other or unknown

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other or unknown

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other or unknown

NAME/KEY: modified base LOCATION: (114527)...(114626)

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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                             Sequence
          APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                    APPLICANT:
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OTHER INFORMATION: a, t, c, o
NAME/KEY: modified base
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LOCATION: (192158)
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LOCATION: (164710)..(164809)
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OCATION: (164700)
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LOCATION: (153242)...(153341)
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Koulu, Markku
Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
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Salonen, Riitta
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Alhopuro, Pia
                                                                                                                                                              Tuomainen, Tomi-Pekka
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"nen, Kristina
NUMBER: 09/422,985
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RESULT 10
US-09-728-444-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 146, Application US/09728444 Patent No. US20020161207A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
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                                                  APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Archur T.
APPLICANT: Sands, Archur T.
TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 146
                                      NUMBER OF SEQ ID NOS: 1206
                                                                                                                                                                                                                                  APPLICANT: Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)..(1341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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42; Conservative
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93.3%;
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Sequence 124, Application US/09728444
Patent No. US20020161207A1
GENERAL INFORMATION;
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020161207A1e1 Murine Polynucleotide Sequences
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
PRIOR APPLICATION NUMBER: US/09/728,444
PRIOR APPLICATION NUMBER: US/01-30
PRIOR APPLICATION NUMBER: US/01-30
PRIOR APPLICATION NUMBER: US/01-30
PRIOR FILING DATE: 1909-11-30
PRIOR FILING DATE: 1909-12-0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1420, Application US/09728446
Patent No. US20020081668A1
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020081668A1el Must
FILE REFERENCE: LEX-0101-USA
CURRENT APPLICATION UNMBER: US/09/728,446
PRIOR APPLICATION UNMBER: US/09/728,446
PRIOR APPLICATION UNMBER: US/09/728,446
PRIOR APPLICATION NUMBER: US 60/168,270
PRIOR FILING DATE: 199-12-01
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 234
TYPE: DNA
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US-09-728-444-124
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FEATURE:
FEATURE
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; LOCATION: (1)...(223)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-146
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Best Local Similarity 89.6%;
Matches 43; Conservative
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Pred. No. 0.013;
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Pred. No. 0.013;
0; Mismatches
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Mutant Animals Defined Thereby
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                                                                                                        APPLICANT
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RESULT 14
US-10-161-927-81
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                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                       APPLICANT:
APPLICANT:
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US-10-425-114-10213
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Best Local :
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SEQ ID NO 10213
LENGTH: 642
TYPE: DNA
                                                                                                                                                                 APPLICANT:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10213, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: 700899387_FLI
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(330)
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                                                                                                                                                                                                                                                                                         231 GAGGÁTGÁGGATGAGGÁTGAGGATGÁGGÁGGÁGGÁGGÁGGÁGGÁAGÁGÁG 278
                                                                                       Shew. Miller, Cum. Hight, Tord Hight, Tord High Tord L. Talente L. Jason C.
                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                            43;
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Gangolli, ku...
Gangolli, ku...
Corine
                                                                                                                                                                                           Zerhusen, Bryan D.
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        Pena, Carol E.A.
Gorman, Linda
Anderson,
                                               Padigaru, Muralidhara
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                                                                                                                                                                                                                     Application US/10161927
To. US20030235821A1
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Similarity 89.6%;
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rolli, Esha A.
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                                                                                                                                       , Kimberly A., Suresh G., Charles E.
                                                                                                                                                                                                                                                                                                                                                          78.4%; Score 40; DB 12; Length 642; 89.6%; Pred. No. 0.012;
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Pred. No. 0.013;
0; Mismatches
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Anderson, David W. Edinger, Shlomit R.

Patturajan, Meera

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(1166)
US-10-161-927-81
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 81
LENGTH: 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR EPILING DATE: 2002-06-03
PRIOR EPILICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR ADDITATION NUMBER: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stone, David J.

TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-377 D (Cura 677 Other)
CURRENT APPLICATION NUMBER: US/10/161,927
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zerhusen,
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                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-09-27
APPLICATION NUMBER: 60/299,133
FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/298,528
FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/325,685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/297,414 FILING DATE: 2001-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-06-06
APPLICATION NUMBER: 60/296,575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/297,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-06-07
T: Edinger, Shlomit R.
T: Patturajan, Meera
T: Stone, David J.
INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                           Miller, C. Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                     Spytek, Kimberly A. Shenoy, Suresh G.
                                                                                         Anderson, David W.
                                                                                                         Gorman, Linda
                                                                                                                                                                             Gangolli, Esha
Vernet, Corine
                                                                                                                                                                                                                                Baumgartner, Jason C.
                                                                                                                                                                                                                                                    Gerlach, Valerie L.
                                                                                                                                                            Padigaru, Muralidhara
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                                                                                                                          Carol E.A.
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89.6%;
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Pred. No.
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0.012;
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                       THEM AND METHODS
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US-10-424-599-47976
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; LOCATION: (1)..(1141)
US-10-161-927-83
                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_143329C.1
US-10-424-599-47976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47976, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 47976
                                                                                          Query Match
Best Local
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LENGTH: 1178
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Best Local
                                                                           Matches
                                                                                                                                                                                                                                                                                                       APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules J
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 21402-377 D (Cura 677 Other)
CURRENT APPLICATION NUMBER: US/10/161,927
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
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PRIOR APPLICATION NUMBER: 60/298,528
PRIOR FILING DATE: 2001-06-15
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PRIOR APPLICATION NUMBER: 60/297,567
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PRIOR APPLICATION NUMBER: 60/296,575
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PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
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PRIOR FILING DATE: 2001-09-27
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                                                                                                                                                                                          ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                   TYRE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                        LENGTH: 1290
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                                    Similarity
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43; Conservative
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                                                                                              78.4%;
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Pred. No.
                                                                                              Score 40; DB 12
Pred. No. 0.012;
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                                                                                                                DB 12; Length 1290;
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APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Hishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Ecoshkin, Alexey M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILLE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
NUMBER OF SEO ID NOS: 8603
                                                                                             , ORGANISM: Aspergillus fumigatus
US-10-128-714-6204
         Query Match
Best Local Similarity 89.6
43; Conservative
                                                                                                                               NUMBER OF SEQ ID NOS: 863
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6204
LENGTH: 2367
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-014-B11_FLI
US-10-425-114-19415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6204, Publication No.
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APPLICANT: Screen, Steven E
APPLICANT: Cao, Yorgwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 19415
SEQ ID NO 19415
TYPE: NM433
TYPE: NM433
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US-10-425-114-19415
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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o. US20030119013A1
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                                     78.4%;
89.6%;
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89.6%;
               0; Mismatches
                    Score 40; DB 14; Length 2367; Pred. No. 0.012;
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Pred. No. 0.012;
0; Mismatches 5; Indels
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Best Local s
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RESULT 22
US-10-225-068-65
; Sequence 65, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
LOCATION: (31)..(2427)
; OTHER INFORMATION: G1089
US-09-934-455-177
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SEQ ID NO 47
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                        Query Match
Best Local
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SEQ ID NO 177
                                                                                                                                                                                                          Matches
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Publication No. US20030121070A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant
FILE REFERENCE: MBI-0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
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                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                      865 GATGACGAAGATGAGGAGGAGGAAGAGGAGGAAGAGGAGGAAGAG 912
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                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                          43; Conservative
                                                                                                                                                                                                                          Similarity
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Jiang, Cai-Zhong
Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dubell, Arnold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reuber, Lynne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Biotechnology, Inc.
                                                                                                                                                                                                                        78.4%;
89.6%;
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                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                        Score 40; DB 10;
Pred. No. 0.012;
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TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND TITLE OF INVENTION: POLYPEPTIDES IN PLANTS FILE REPERENCE: 51444202040
CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-108-09
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,649
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
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APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samaha, Raymond
APPLICANT: Pilgrim, Marsha
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/9/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/120,880
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
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US-10-302-267-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 2663
TYPE: DNA
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APPLICANT:
APPLICANT:
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Local Similarity 89.6%; Pred. No.
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Reuber, Lynne
Zhang, James
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Fromm, Michael
Heard, Jacqueline
Heard, Jose Luis
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Broun, Pierre E.
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Adam, Luc
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APPLICANT: YL, Guo-Liang
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-08
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 09/934,455
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publication No. US20040019927A1
GENERAL IMPORMATION.
APPLICANT: Sherman, Bradley K
APPLICANT: Sherman, Jose Luis
APPLICANT: Heard, Jacqueline B
APPLICANT: Heard, Jacqueline B
APPLICANT: Haake, Volker
APPLICANT: Hake, Volker
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Retuber, T. Lynne
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Broun, Pierre B
APPLICANT: Didgim, Marsha L
APPLICANT: Didgim, Marsha L
APPLICANT: Didgim, Marsha L
APPLICANT: Didgim, Marsha L
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SEQ ID NO 45

LENGTH: 2663

TYPE: DNA

ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2424)

OTHER INFORMATION: G1089

US-10-302-267-45
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PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
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Best Local Similarity 89.0
43; Conservative
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PRIOR APPLICATION NUMBER: 60/129,450
PRIOR APPLICATION PRIOR PRIOR
                                                                                                                                                                                                                  APPLICATION NUMBER: 60/338,692
FILING DATE: 2001-12-11
APPLICATION NUMBER: 10/171,468
FILING DATE: 2002-06-14
APPLICATION NUMBER: 10/225,066
                                                                                                                           APPLICATION NUMBER: 10/225,067
FILING DATE: 2002-08-09
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Broun, Pierre E
Pilgrim, Marsha L
Dubell III, Arnold
Pineda, Omaira
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89.6%; Pred. No. 0.
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APPLICANT: HI, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zandidio, Carlos
APPLICANT: Lemieux, Sebassien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
CURRENT FILME NETS: 10182-018-99
CURRENT PAPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US/00/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-99
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08
                                                                                                                                                                                                                                                                                       RESULT 26
US-10-128-714-5204
                                                                                                                                                               Sequence 5204, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
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US-10-128-714-204
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; OTHER INFORMATION: G1089
US-10-374-780A-229
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Best Local
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NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 43; Conserv
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ORGANISM: Arabidopsis thaliana
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D: US20030119013A1
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89.6%;
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Pred. No. 0.011;
0; Mismatches 5; Indels
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RESULT 28
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-5204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-029-386-17979/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17979
LENGTH: 191
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                               Best Local
                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/287;066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO CHR22_81.0
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
OTHER INFORMATION: NT HIT: 916168503, EVALUE 2.00e-31
OTHER INFORMATION: EST_HUMAN HIT: BE392547.1, EVALUE 2.00e-32
OTHER INFORMATION: SWISSPROT HIT: P46060, EVALUE 2.00e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Bapiens
FEATURE:
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                                                                                                                                                                                               Similarity
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                                                                                     Lemieux, Sebastien M
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                                                                                                                                                                                               76.5%;
89.4%;
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89.6%;
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Pred. No.
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Pred. No.
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US-09-864-761-18355
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OTHER INFORMATION: EXPRESSED IN HELA, 0
OTHER INFORMATION: EXPRESSED IN BONE M
OTHER INFORMATION: EXPRESSED IN LUNG, 0
OTHER INFORMATION: EXPRESSED IN ETTAL 1
OTHER INFORMATION: EXPRESSED IN HEATN,
OTHER INFORMATION: EXPRESSED IN HEATN,
OTHER INFORMATION: EXPRESSED IN BEAIN,
OTHER INFORMATION: EXPRESSED IN BEAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18355
LENCTH: 423
TYPE: DNA
  Matches
                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR APPLICATION NUMBER: US 60/207,456
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                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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42;
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Hanzel, David K.
Chen, Wensheng
  Conservative
                                                                                                                     N: EXPRESSED IN HBL100, SIGNAL = 3.1

N: EXPRESSED IN HELA, SIGNAL = 2.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

N: EXPRESSED IN LUNG, SIGNAL = 1.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 1.9

N: EXPRESSED IN PLACENTA, SIGNAL = 1.9

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

N: EXPRESSED IN BT474, SIGNAL = 2.2
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                       76.5%;
89.4%;
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                          Score 39; DB 9;
Pred. No. 0.024;
  Mismatches
                                                  Length 423
  Indels
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Search completed: February 29, 2004, 22:23:53
Job time : 211 secs
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US-10-029-386-4279/c
Sequence 4279, Appl:
Publication No. US20
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APPLICANT: Penn, Sharron G.

APPLICANT: Annk, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PILLE REFERENCE: ABOMICA, X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                 Matches
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Best Local :
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
OTHER INFORMATION: SWISSPROT HIT: P46060, EVALUE 1.00e-06
OTHER INFORMATION: EST HUMAN HIT: BE392547.1, EVALUE 5.00e-33
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Best Local Similarity 89.4
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                LENGTH: 543
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                     42;
                                                                                                                                         Similarity
                                                GÁGGÁAGÁTGAGGÁÁGÁÁGÁÁGÁÁGÁÁGÁÁGÁÁGGÁÁGÁÁGÁÁGÁÁGÁ
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                                                                                                                            Conservative
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._US20030194704A1
                                                                                                                76.5%; Score 39; DB
89.4%; Pred. No. 0.02
tive 0; Mismatches
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89.4%;
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Pred. No. 0.024;
0; Mismatches 5; Indels
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Listing first 150 summaries
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Perfect score:
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   Pred.
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the number of results predicted by chance to have
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SUMMARIES

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Location/Qualifiers
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1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.

Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization J. Biol. Chem. 276 (7), 4917-4922 (2001)
                                 Homo sapiens BAC clone
AC092603 AC073396
AC092603.2 GI:16303539
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                                                                                                                                                                                          GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG
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sapiens (human)
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDHODPYSVQATAAIAAITFLILFTIFGNALVILAUTISRSLR
APQNLFLVSLAAADILVATLI FPSLANELLGYWYFRRTWCEVYLALDVLFCTSS IVH
LCAISLDRYMAVSRALEFYNSKRTFRRIKCIILTVWLIALAVISLPPLIYKGDQGFQBFG
RPQCKLNQBAWYILASSIGSFFAPCLIMILVYLRIJLLAKRSKNRRGFBAKGGFQQGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKETGEKEEGETPEDTGTRALPFSWAA
LPNSGQGQKKEGVCGASPEDDALEEEEEEECGEPQAVFVSFASACSPPLQOPQGSRVAA
LPNSGQGOKKEGVCGASPEDDALEEEEEEECGEPQAVFVSFASACSPPLQOPQGSRVAA
TLRGQVLLGRGVGAIGGQWMRRRAQITREKRFTFVLAVVIGVFVLCWFFFFSYSLGA
                                                                                                                                                                                                                                                                                                                                                                                 Accession Number AF005900; polymorphic sequence lack three glu residues at this location" /frequency="Caucasians 0.31; African-Americans 0.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="alpha_2B_adrenergic_receptor"
/protein_id="AAK01635.1"
/db_xref="GI:12698670"
                                                                                                                                                                                                                                                                                                                                                                replace="gaagaggag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ADRA2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="ADRA2B"
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/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         note="compared to wild type sequence
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                                       GI:16303539
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_xref="taxon:9606"
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Pred. No. 7e-
0; Mismatches
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RP11-139J6
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7e-05;
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                      MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
Mo. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such from more than one subclone; all regions were covered by sequence from the sequence subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Oct 20, 2001 this sequence version replaced gi:14916188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO 63108, USA
5 (bases 1 to 22842)
Waterston,R.H.
Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (20-OCT-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-UUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 4 (Dases 1 to 22842)
Waterston, R. H.
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The sequence of Homo sapiens
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhini losses I to 22842)
Sulston, J. E. and Waterston, R. Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sapiens@watson.wustl.edu
Summary Statistics
Center project name: H_NH0139J06
Drafting Center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
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piens BAC clone RP11-139J6
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4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphisms have been identified between AC013272 and AC092603.
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VECTOR: pBACe3.6
                                                                                                                                                                                                   /rpt
12062
                                                  'note="match to EST
                                                                                                                                                                                                                                          / TPC family="MIR" 11617. .11882
                                                                                   note="match to EST AI791589
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                                                                                                                                     note="match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="(GGCTG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L2"
7278. .7415
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1377. .1424
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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      EST BF475329
                                              BF475329
(NID: 911546156) "
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                                       (NID:g11546156) "
                                                                      (NID:g5339305) oj40h05.y5
                                                                                                             (NID: 93002438) oj40h05.sl"
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REFERENCE AUTHORS TITLE

Waterston, R.

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE JOURNAL

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JOURNAL MEDLINE

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ORGANISM

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AUTHORS
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                                                                                                                                                                                                                                                                                          Phoca vitulina partial aar2B gene
                                                                                                                                                                                                                           aar2B gene; alpha adrenergic receptor Phoca vitulina (harbor seal) Phoca vitulina
                              Madsen, O.
                                                                                                                                               Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adkins,R., Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae;
                                                                                             Nature 409 (6820), 610-614 (2001)
                                                                                                                              Parallel adaptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                               (bases 1 to 1168)
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                  Submission
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14762. 14822
/note="similar to Homo sapiens E(
(NID:g12877089)"
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14060. .14247
(18-NOV-1999) Madsen O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match to EST AA836522 (NID:g2910841) od22d08.sl"
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/note="match to EST AA830781
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(NID:g8082456)"
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(NID:g12886265)"
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Pred. No. 6.3e-05;
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Department of Biochemistry,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lama pacos partial adra2b gene adra2b-2 allele.
                                                                                                                                                                             Submitted (14-AUG-2002) Madsen O., 161 Biochemistry NWI, University of Nijmegen, PO.BOX 9101, 6500HB Nijmegen, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                               Madsen,O., Willemsen,D., Ursing,B.M., Arnason,U. and de Jong,W.W. Molecular evolution of the mammalian alpha 2B adrenergic receptor Mol. Biol. Evol. 19 (12), 2150-2160 (2002) 22337198
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
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adra2b gene; alpha 2B adrenergic receptor
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                                'gene="adra2b"
                                                                                                                            organism="Lama pacos"
                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                .1180
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                                                                                               l_type="genomic DNA
_xref="taxon:30538"
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Pred. No. 0.0017;
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MAM 12-DEC-2002

U. and de receptor

Jong, W.W.

Length 1168; Indels

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Query Match
Best Local Similarity 90.2
46; Conservative
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Submitted (14-AUG-2001) Madsen O., 161 Biochemistry NWI, University of Nijmegen, P.O.Box 9101, 6500 HB Nijmegen, NETHERLANDS
1. .1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 GAGGAGGAGGCTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCCTCAG 895
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Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
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/db_xref="SPTREMBL:08MKS1"
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/ L'ATRI RE LONE "ALAVITELIL FTI FGNALVILAVLTSRSLRAPQNLFLVSLAAA |
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LLGRGVCTSRGQWWRRRAQLTREKRFTFVLAVVIGVEVLCWFPFFFFSYSLGAI CPEHC
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<1. .>1197
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Pred. No. 0.014;
0; Mismatches
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adrenergic receptor.
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Best Local Similarity 90.2
46; Conservative
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                                                                    43;
                                                       Similarity 95.6
43; Conservative
GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAAGTGTGAA 45
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Diagnosis of behavioural disorders, neurological disorders
                                                                                                                                                                                                                                                                                                                              synthetic construct
synthetic construct
artificial sequences.
                                                                                                                                                                                                                                          Patent: WO 0202809-A 5 10-JAN-2002;
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Sequence 5 from Patent WO0202809.
AX348497
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Sequence 47 from Patent
AX344976
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                                                                    82.0%;
95.6%;
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90.2%;
                                              Score 41.8; DB
Pred. No. 0.03;
0; Mismatches
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Pred. No. 0.014;
0; Mismatches
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**system** 

PAT 01-FEB-2002

PUBMED REFERENCE AUTHORS TITLE

11743200

JOURNAL MEDLINE

TITLE

REFERENCE AUTHORS

KEYWORDS SOURCE DEFINITION ACCESSION VERSION

ORGANISM

RESULT 8 LPA315941

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Original source text: Human adult ne Draft entry and computer-readable se kindly submitted by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience 155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             610
                                                                                                                                                                                                                                                                                       1 (bases 1 to 885)
Chang, A.C., Ho, T.F. and Chang, N.C.
Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in
                                                                                     Homo sapiens
NB1-818S.
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AJ325747.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M38742.1
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/product="alpha-2-adrenergic receptor"
/protein_id="alpha-2-adrenergic receptor"
/protein_id="alpha-2-adrenergic receptor"
/protein_id="alpha-2-adrenergic receptor"
/db_xref="GDB:GOO-120-540"
/db_xref="GDB:GOO-120-540"
/db_xref="GDB:GOO-120-540"
/db_xref="GDB:GOO-120-540"
/db_xref="GDB:GOO-120-540"
/db_xref="GI:177868"
/db_xref=
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4p16.3-p15"
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                                                                                                             genomic sequence
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91.7%;
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_type="neuroblastoma"
ue_type="neural"
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Sequence 1 from Patent WO0179561.
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1 (bases 1 to 1030)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R. Nott Lanking sequences: a tool for gene discovery and verification
                                                                                                                                                                                                                                                                                            Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zabarovsky, E.R.
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nilarity 91.7%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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Box 280, Stockholm 171 77,
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HUMADRA2RA
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Draft entry and computer-readable sequence for [1] kindly submitted
by J.W.Lomasney, 03-MAY-1990, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo... 1 (bases 1 to 2072)

Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.

Expansion of the alpha 2-adrenergic receptor family: cloning and the gene for which is located on chromosome 2 eroc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-2-adrenergic receptor; plasma membrane protein; receptor-coupled G protein.
Homo sapiens (human)
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1 (bases 1 to 2072)
Au-Young, J. and Seilhamer, J. J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AR270618
AR270618.1
/Protein_id="Aaa51666.1"
/ db_xref="01:178198"
/ db_xref="01:178198"
/ db_xref="01:178198"
/ db_xref="01:178198"
/ translation="widhqupsyvoataalaaaltfiletiletilegnalvilavltsrslr
/ translation="widhqupsyvoataalaaaltfiletilegnalvilavltsrslr
APQNLFUSI.AAADILVATL1IPFSLANELLGYMYPERTWCEVYLALDVLFCTSSIVH
RPQCKLNQBAWILLASSIGSFRAPCLIMILVVIRITAVVISLPFLIYKODQSBPBRG
KOPREDHGGALASAKLPALASVASAREVNGHSKSTOEKEBGETPEDTGTRALPPSWAA
VLATLRGOVYLLGREVGALGSOMWRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSYS
VLATLRGOVYLLGREVGALGSOMWRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAM
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2-adrenergic receptor (alpha-2
                                                                                                                                                                            /note="alpha-2-adrenergic receptor (alpha-2 C2)
                                                                                                                                                                                                                        /gene="ADRA2B"
                                                                                                                                                                                                                                                  'gene="ADRA2B"
                                                                                                                                                                                                                                                                              mol_type="ye.....9606"
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|mol_type="genomic DNA"
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4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG 51
                           Conservative
                                 81.6%;
91.7%;
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                               Score 41.6;
Pred. No. 0
                      Mismatches
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                                 Length 2072;
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                  Gaps
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Patent: WO 02061087-A 41 08-AUG-2002; Lifespan Biosciences, Inc. (U Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. /organism="Homo sapiens" /mol\_type="unassigned DN /db\_xref="taxon:9606" 41 from Patent GI:25813686 3274 bp [ : WO02061087. DNA" DNA linear PAT 26-NOV-2002

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ORIGIN

4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG GĀĀGĀGGĀĀGĀĀĢĀĀĢĀĀĢĀĀGĀĀĢĀĀĢĀĀĢĀĀĢĀĢTĢTĢĀĀČČČĆĀĢ 939 81.6%; ilarity 91.7%; Conservative Score 41.6; D Pred. No. 0.03 0; Mismatches 0, .035; DB 6 4. Length 3274; Indels 51 0, Gaps 0;

JOURNAL CHU Rangueil, Toulouse 31403, France
3 (bases 1 to 9944)
Cayla, C., Heinonen, P., Viikari, L., Schaak, S., Snapi
Bouloumie, A., Karvonen, M., Pesonen, U., Scheinin, M. Direct Submission Submitted (29-MAY-1997) INSERM Unit 317, 2 (bases 1 to 9944)
Cayla, C., Schaak, S., Bouloumie, A., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 9944)

Cayla, C., Helmonen, P., Vilkari, L., Schaak, S., Snapir, A., Alpha2C2-adrenergic receptor gene Cayla, C., Heinonen, P., Viikari, L., Sch. Bouloumie, A., Karvonen, M., Pesonen, U., AF005900.2 GI:33439705 (05-AUG-2003) INSERM Unit 317, Institut Louis Bugnard, 9944 bp DNA linear PRI 05-alpha2B-adrenergic receptor (alpha2C2AR) gene, Devedjian, J.C. and Paris, H.Schaak,S., Snapir,A., ,U., Scheinin,M. and Paris,H. Institut Louis Bugnard Snapir, A and Paris, H. PRI 05-AUG-2003

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Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                  Nycticebus coucang
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
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AJ251186.1 GI:11322429
Bar2B gene; alpha adrenergic receptor
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Sequence update by submitter
On Aug 5, 2003 this sequence version replaced gi:2245627.
                                                                                                                            Submitted (18-NOV-1999)
University of Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nycticebus
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APQNLFLVSLAAADILVATLIIPSLAKABLLGYWYERRYWCEVYLALDVLFCTSSIVH
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RPQCKLNQEAWYILASSIGSFFAFCLINILVYLRIYLLAKRSNRRGPRAKGGPCGGES
KQPRDHGGALASAKLFALASVASAREVNGHSKSTGEKEEGETPETTCTRALPPSWAA
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/organism="Nycticebus coucang"
/mol type="genomic DNA"
/db xrefe="taxon:9470"
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VLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="alpha2B-adrenergic receptor"
/protein_id="AAB62558.1"
/db_xref="GI:2245628"
                                                                                           Location/Qualifiers
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/note="alpha2C2 ad
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/db_xref="taxon:9606"
/chromosome="2"
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|mol_type="genomic DNA"
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                                                                                                                              Madsen O., Department of Biochemistry, P.O. box 9101, 6500 HB Nijmegen,
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Douzery, E.J.P.

Direct Sub--/
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences (l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J., Catzeflis,F., de Jong,W.W. and Douzery,E.J. Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
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A2AB gene; alpha 2B adrenergic receptor.
Thomomys talpoides (northern pocket goph
Thomomys talpoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Douzery, E.J.P., Delsuc, F., Stanhope, M.J. and Huchon, D. Local molecular clocks in three nuclear genes: diverge rodents and other mammals, and incompatibility among f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Sciurognathi; Geomyidae;
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AJ427262
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Thomomys talpoides partial A2AB
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F"
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| fossil
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Query Match
Best Local Similarity
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3 (bases 1 to 1179)
Douzery, E.J.P.
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Local molecular clocks in three nuclear genes: divergence times
rodents and other mammals, and incompatibility among fossil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huchon, D., Madsen, O., Sibbald, M.J., Ament, K., Stanhope, M.J., Catzeflis, F., de Jong, W.W. and Douzery, E.J.

Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear genes Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A2AB gene; alpha 2B adrenergic receptor.
Trichye fasciculata (long-tailed porcupine)
Trichye fasciculata
Trichye fasciculata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hystricidae; Trichys.
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Pred. No. 0.041;
0; Mismatches 6;
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Gene for alpha 2B adrenergic
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AUTHORS
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ORGANISM
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VERSION
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JOURNAL REFERENCE AUTHORS TITLE

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TITLE

REFERENCE AUTHORS

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VERSION KEYWORDS SOURCE

ORGANISM

ACCESSION DEFINITION RESULT 20 TFA427266 LOCUS

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Matches

ORIGIN

exon

FEATURES

source

gene

SdC

Query' Match

76.18;

Score 38.8;

DB 10;

Length 1347;

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Query Match
Best Local :
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Submitted (26-DEC-2000) Pharmacology, University of Colorado Health Sciences Center, 4200 East Ninth Ave C236, Denver, CO 80282, USA
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Ehringer, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Canniff, J., Beneson, M., Gordon, L., Bennett, B., Johnson, T.E. and Sikela, J.M. High-throughput sequence identification of gene coding variants within alcohol-related QTLs
Mamm. Genome 12 (8), 657-663 (2001)
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AICPOHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                  'gene="Adra2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol
                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="AIAAVITELILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAA DILVATLIPESLANELLGYWYFRRIWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS RALEYNSKETERRIKCIILTVWLIAAVISLEPLVYKODGGPQFHGRPQCKLNQEAWYI LASSIGSFFAPCLIMILVYLRIYLLAAVISLEPLVYKODGGPQFHGRPQCKLNQEAWYI DKVFTLASPSSAGBANGRPKFTGEKEEGETPEDPGTRPLFPSWAALPSSGQDQKKGY GAVGGQWWRRRTQATASCEPQAVAVSPASGCSPTLQQPQGSRVLATLRGQVLLGRGV GAVGGQWWRRRTQMTREKRFTFVLAVVIGVFVLCWFFFFSVSLGAICPQHCKVPHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=1
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/gene="A2AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.0%;
86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.8; DB 10;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1347 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROD 21-FEB-2002
B (Adra2b) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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L00979.1 GI:191547

2-C2

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RESULT 23
MUSAADRENH
LOCUS
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AUTHORS
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AF332050
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VERSION
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                                  DEFINITION
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 ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snoor
                                                                                                                                                                                                        Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                       883
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Mus musculus :
complete cds.
AF332050
AF332050.1 G
                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGATGTGAACCCCA
                                                                                                                                                                                                            43;
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                                MUSAADRENH
Mus musculus alpha-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
Sciences (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1347)
Ehringer,M.A., Thompson,J., Conroy,O., Xu,Y.,
Beeson,M., Gordon,L., Bennett,B., Johnson,T.E.
complete cds.
L00979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High-throughput sequence identification within alcohol-related QTLs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beeson, M., Gordon, L., Bennett, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehringer, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11471062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21363810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCA
                                                                                                                                       GAGAAGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1347)
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome 12 (8),
                                                                                                                                                                                                                                                                                        /product="adrenergic receptor alpha 2B"
/protein_id="AAK56079.1"
/protein_id="AAK56079.1"
/db_xref="Gi:14193668"
/translation="MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSIR
/translation="MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSIR
/translation="MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSIR
/translation="MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSIR
/translation="MVHQEPYSVGATARIKCIILITVMLIAAVISIPPLIXYEDQARRGSGEGE
LPQCELNQEAWYILASSIGSFFAPCLIMILVYLRIYVIAKRSHCRGLGAKRGSGEGES
KKPHPAAGGVPASAKVPTLVSPLSSVGEANGHFKPPREKEEGETPEDDEARALPPNWS
ALPRSVQDQKKGTSGATAEKGAEEDDEEEVEECEPQTLAFSPASVFNPPLQQPQTSRVL
ATLRGQVLLSKAVGVASGQWWARRTQLSREKR ETFVLAVVIGVEVVCWFPPFFSYSLG
AICPQHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (26-DEC-2000) Pharmacology, University of Colorado Health
Center, 4200 East Ninth Ave C236, Denver, CO 80262, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Adra2b"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="Adra2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain-"ILS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:14193667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain
                                                                                                                                                                                                                         76.1%;
86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SII
                                adrenergic
                                                                                                                                                                                                      Score 38.8; DB Pred. No. 0.23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           657-663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.23
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenergic
                                                  1650 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conroy,O., Xu,Y., Yang,F., Canniff,J., tt,B., Johnson,T.E. and Sikela,J.M. entification of gene coding variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                DNA linear ROD 27-
receptor (Malpha2-2H) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
r alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang, F., Cann.
. and Sikela, J
                                                                                                                                                                                                                                            1347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 21-FEB-2002
3 (Adra2b) mRNA,
                                                    ROD 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 932
                                                                                                                                                                         50
                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canniff,J
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
RATA2BR
LOCUS '
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MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION ACCESSION
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                                                                                                                                       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                      JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1109 GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA 1158
                                                                                                                                                                      1 (bases 1 to 2319)
Zeng, D.W., Harrison, J.K., D'Angelo, D.D., Barber, C.M., Tu
Lu, Z.H. and Lynch, K.R.
Molecular characterization of a rat alpha 2B-adrenergic
Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990)
90222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
92378586
                                                                                                                     Original source text: Rat (strain cDNA to mRNA, clones dz-(3,5,6).
                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenergic receptor Biochem. Biophys. Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                    Draft entry and computer-readable K.R.Lynch, 12-FEB-1990.
                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                  adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                    M32061.1 GI:202589
                                                                                                                                                                                                                                                                                                                                                                                                      M3206:
                                                                                                                                                                                                                                                                                                                                                                                                                     Rat alpha-2B-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                        RATA2BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kobilka, B.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chruscinski, A.J., Link, R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-2 adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1354956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                   R.Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVHQEPYSVQATAAIASAITFLILPTIFGNALVILAVLTSRSLR
APQNLFUNGLAADILVATLIIEFSLARELGYWYFWRAWCEVYLALDVLFCTSSIVH
LCAISLDRYMAVSRALEFYNSKRTPRAIKCIILTVWLIAAVUSLPPLIYKGDQREEPHG
LPQCELNQEAWYILASSIGSFFAPCLIMILVYLRIYVIAKRSHCRGLGAKRGSGEGES
KCRPRAAGGYPASAKVPTLVSPLSSVGEANGHFKFPREKEEGETPEDDEARALFPNWS
ALPRSVQDQKKGTSGATAEKGAEEDDEEEVEGCEPQTLFAFBASVFNPFLQQPQTSRVL
ATLRGQYLLSKNVGNASGQWWRRRTQLSREKRETFYLAVVIGVEVVCWFPFFFSYSLG
AICPQHCKVPHGLFQPFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source text: Mus mu
Location/Qualifiers
                                                                 Location/Qualifiers
organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="alpha-2 adrenergic receptor"
/protein_id="AAA37131.1"
/db_xref="GI:191548"
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strain="129/Sv"
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86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     2319 bp
receptor
                                                                                                                                                                                                                                                                                                                                                   rat)
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(RNG-alpha-2) mRNA,
                                                                                                       sequence
                                                                                                                                     Sprague Dawley) adult kidney,
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    kindly submitted

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                                                                                                                                                                                                                                              Tucker, A.L.,
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1 (bases 1 to 6268)
Schaak,S., Cussac,D. and Paris,H.
Cloning and characterization of the rat alpha2B-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-MAR-2001) U388,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 6268)
Schaak, S., Cussac, D. and Paris, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus alpha2B-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGGAAGAGTGTGAACCCCA 50
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                                                      /product="alpha2B-adrenergic receptor"
2408. 2779
/gene="Rmg"
/note="5'UTR"
                                                                                                                                                                                                       /gene="Rng"
2408. .5989
                                                                                                                                                                       gene="Rng"
                                                                                                                                                                                                                                                     'gene="Rng"
                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="there is no consensus sequence for N-linked 91yoosylation (NXS/T) in this receptor"
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/product="alpha-2B-adrenergic receptor"
/protein_id="AAA40635.1"
/db_xref="GI:202590"
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/dev_stage="adult"
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Pred. No. 0.22;
0; Mismatches
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Sciurognathi; Muridae;
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. 22;
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; Murinae;
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AUTHORS
TITLE
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PUBMED
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AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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MUSADRRECA
LOCUS
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Best Local Similarity
Matches 43; Conserv
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Chang, A.C.
Direct Submission
Submitted (24-MAY-2002) Neuroscience, National Yang-Ming
University, 155, sect. II, Li-Noon St., Taipei, Taiwan 112,
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                                                                                                                                                                                                  Chang, A.C.
Direct Submission
Submitted (27-APR-1993) Neuroscience, National Yang-Ming
University, 155, sect. II, Li-Noon St., Taipei, Taiwan 112,
                                                                                                                                                                                                                                                                                                                                                                                          Chen, W.M., Chang, A.C., Wang, C.M., Lin, C.C. Characterization of the regulatory regions adrenoceptor subtype gene
Neurosci. Lett. 210 (1), 33-36 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, W.M., Chang, A.C., Shie, B.J., Chang, Y.H. and Chang, N.C. Molecular cloning and characterization of a mouse alpha 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adrenoceptor subtype gene
Biochim. Biophys. Acta 1171 (2), 219-223 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 9377)
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                                                                                                                                                                          (bases 1 to 9377)
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SRSLHAPQNLFUVSLAAADILVATLIIPFSLANELLGYWYFWRAWCEVYLALDVLFCT
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SSIVHLCAISLDRYWAVSRALEYNSKRTBFRRIKGIILIVYLRIYVIAKRSHCRGLGAKRGS
PEPRGLPQCELNQEAWYILASSIGSFFAPCLLMILVYLRIYVIAKRSHCRGLGAKRGS
PEPTWAFLPRSGQGOKKGTSGATAEEGDEEDEEDVERSCEEDVILPASPASVCNPPPLOOPQ
TSRVLATLRGQVLLGKWYGVASGQOWMRRRTQLSREKRFTFVLAVVLGVFVFVVCWFPPFP
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TSRVLATLRGQVLLGKWYGVASGQOWMRRTGDLSREKRFTFVLAVVLGVFVVCWFPPFP
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/gene="Rng"
/note="3'UTR"
5907
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/gene="Rng"
/note="polyA_signal"
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86.0%;
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2 adrenergic
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                               and Chang, N.C. of murine alpha 2C2
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٥,
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JOURNAL REFERENCE AUTHORS TITLE

Unpublished

FEATURES

France

source

mRNA 5'UTR

gene promoter

JOURNAL

REFERENCE AUTHORS

Rattus

TITLE

SOURCE ORGANISM

**EYWORDS** 

ACCESSION VERSION

AF366899 AF366899.1

RESULT 25 AF366899 LOCUS

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1263

ORIGIN

Query Match Best Local Similarity

Matches

43;

DEFINITION

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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VERSION
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AL731836
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Best Local Similarity
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Cambridgeshire, CBIO ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 30, 2002 this sequence version replaced gi:21104241.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeates; all regions were covered by at least
one plasmid subclone or more than one MI3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6161 GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGAGGAAGAATGTGAACCCCA 6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>3</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAY-2002) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL731836
AL731836.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL731836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Love
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               мау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 83802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24, 2002 this sequence version replaced gi:927107.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSGPAMVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLT
SRSLRAPQNLFLYSLAAADILVATLIIPSLANELLGYMYFMRAMCEVYLALDVLFCT
SSIVHLCAISLDRYMAVSRALENNSKRTFRRIKCIILTWILIAAVISLPPLIYKGDQR
PEPHGLPQCELNQEAWYILASSIGSFFAFCLIMILVYLRIYLIAKRSHCREGETFEDPEAR
GEGESKKPRPGFFAAGGVPASAKVPTLVSPLSSVGEANGHPKPPREKEGETFEDPEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6626. .9377
8297. .8932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="alpha-2C2 adrenergic receptor" 4839. .5257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQTSRVLATLRGQVLLSKNVGVASGQWWRRRTQLSREKRFTFVLAVVIGVFVVCWFPF
FFSYSLGAICPQHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPPNWSALPRSVQDQKKGTSGATAEKGAEEDEEEVEECEPQTLPASPASVFNPPLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="alpha-2C2 adrenergic receptor"
/protein_id="AAA73895.1"
/db_xref="GI:927108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="DBA/2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:21264639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%;
86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9_type="liver"
.9377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.8; DB Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83802 bp DNA linear ROD 30-MAY-2002
n clone RP23-119A13 on chromosome 2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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REFERENCE
AUTHORS
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ORGANISM
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AC126878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pocas
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Allen, C., Allen, H., Absrooks, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
Blaiwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Cha, Y., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cookrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dumh, A., Durbin, K., Duval, B., Baves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A.,
Jackson, L., Liu, W., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,
Martin, K., Martin, R., Martinez, B.,
Martin, K., Martin, R., Partez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Parker, K., Parker, A., Perez, A., Perez, L., Pfannkoch, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12506 GAGAAGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA 12555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-119A13 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus clone CH230-263M16, WORKING DRAFT SEQUENCE, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces
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/db_xref="taxon:10090"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="RP23-119A13"
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86.0%;
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Pred. No. 0.
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AL Submitted (15-NOV-2002) Human Geneme Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

The sequence in this assembly is a combination of BAC based reads (http://www.hgc.bcm.tmc.edu/projects/rat/). Each contig Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated exent beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence second will be updated with the finished sequence as a second set is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code, BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conter project name: GZCB
Center project name: GZCB
Center clone name: CH230-263M16
Assembly program: Phrap; version 0.990329
Consensus quality: 114750 bases at least 040
Consensus quality: 115674 bases at least 030
Estimated insert size: 117568; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Submitted (10-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One 3 (Dases 1 to 124474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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ORGANISM
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VERSION
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RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Amuzny, D. M., Adams, C., Ame, J.R., Ayele, M., Banks, T., Babbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Bulabrooks, S. Brieva, M., Brown, E., Brown, M., Bryanin, D., Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, M.C., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Davila, M. L., Davis, C., Davy-Carroll, D., Dathorne, S. R., David, R., Delaney, K.R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H.H., Ealls, T., Ferraguic, D., Edwards, C.C., Elhaj, C., Bscotto, M., Barris, C., Harris, K., Harris, C., Harris, C., Harris, K., Harris, C., Harris, C., Harris, C., Harris, M., Haylak, P., Hale, S., Hamilton, K., Harris, C., Harris, M., Haylak, P., Hale, S., Hamilton, K., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Krashov, L., Korvah, J., Kovar, C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Louise, A., Marrish, R., Lucier, R., Lucier, R., Luna, R., Ma, J., Maris, L., L., Luna, R., Ma, J., Martin, R., Martin, R., Martin, R., Martin, R., Martin, M., Mapua, P., Martin, R., Martin, M., Mapua, P., Martin, R., Martin, M., Luna, R., Ma, J., Martin, R., Martin, R., Martin, M., Luna, R., Ma, J., Martin, M., Lucier, R., Luna, R., Ma, J., Martin, R., Martin, R., Martin, M., Luna, R., Ma, J., Martin, R., Ma
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Rattus norvegicus (Norway rat)
Eukarvora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC091365.5 GI:23664882
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14 unordered pieces.
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clone_end.sps"_
122714 . 124474
/note="wgs_end_extension
clone_end.sps"
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complement(62624. 63503)
/note="clone_boundary
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51753. .53390
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
|mol type="genomic DNA"
|db_xref="texon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%; Score 38.8; D) 86.0%; Pred. No. 0.2; ative 0; Mismatches
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922. .122663
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1e CH230-1A10,
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Center: Baylor

-- Genome Center

COMMENT

Bource

1. .124474

Location

53390: contig of 53390 bp in length 53490: gap of unknown length 124474: contig of 70984 bp in length.

53391 53491

REFERENCE AUTHORS TITLE

JOURNAL

Direct Submission

Rat Genome Sequencing Consortium.

TITLE
JOURNAL
REFERENCE
AUTHORS

JOURNAL

Worley, K.C

(bases 1 to 124474)

TITLE JOURNAL REFERENCE AUTHORS TITLE

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

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AL Submitted (10-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 10, 2002 this sequence version replaced gi:21953942.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, M., Rojas, A., Rojubokan, J., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparke, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Walliamson, A., Meczyk, R., Wooden, S., Wolfrey, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 261258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            table.
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                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                        Center project name: TUEV
Center clone name: CH230-1A10
Center clone name: CH230-1A10
Center clone name: CH230-1A10
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Centensus quality: 19089 bases at least Q40
Centensus quality: 190812 bases at least Q30
Centensus quality: 203158 bases at least Q20
Estimated insert size: 183632; sun-of-centing estimation
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                                                                                                                                                                                                                                                                                                                                            Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
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4484: contig of 4484 bp in length
4584: gap of unknown length
15356: contig of 10772 bp in length
15456: gap of unknown length
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                                                                        Allen, C., Allen, H., Albbrooks, S., Amin, A., Anguiamo, D., Angulamo, D., Anguiamo, D., Balden, H., Albbrooks, S., Amin, A., Anguiamo, D., Badden, H., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Blankenburg, K., Blyth, P., Brown, M., Blankenburg, K., Blyth, P., Brown, M., Charlet, K., Calderon, E., Chacker, C., Charlet, K., Cardens, V., Carter, K., Cavazo, I., Cesazar, H., Center, A., Chen, R., Chen, Y., Chen, Z., Chu, J., Delgado, O., Denson, S., Davy-Carroll, J., De Anda, C., Dederich, D., Delgado, O., Denson, S., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, C., Davy-Carroll, J., De Anda, C., Dederich, D., Deraper, H., Dayis, M., Flagg, M., Forbes, L., Foster, M., Guera, M., Gahisi, A., Ganta, R., Garcia, A., Garrar, T., Garza, M., Gurarandez, S., Finley, M., Flagg, M., Forbes, L., Foster, P., Gebregoovigis, E., Geer, K., Gall, R., Grady, M., Glerra, M., Guevara, M., Harvey, Y., Haylak, P., Hawes, A., Henderson, M., Hernandez, J., Kung, L., Kung,
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
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On Sep 21, 2002 this sequence version replaced gi:21743229.
The sequence in this assembly is a combination of BAC based reads whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the contigs that consist entirely of whole genome shotgun sequence contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently

consists of 2 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
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of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 276543)
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.
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275485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GRPO
Center clone name: GRPO
Center clone name: CH230-46115
Assembly program: phrap, version 0.990329
Consensus quality: 237012 bases at least Q40
Consensus quality: 239346 bases at least Q20
Consensus quality: 240985 bases at least Q20
Estimated insert size: 252028; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.hcm tmc
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/note="clone boundary
clone_end:Sp6
                                  end_sequence:BH330418"
270664. .272163
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note="wgs_end_extension
                                                                                                                                                                                       /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                 'note="clone_boundary
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                                                                                                                                                                                                                                              sequence:BH330415
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lor College of Medicine, One
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Toxicity-

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Maximum DB
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Perfect score:
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1: geneseqn1980s:*
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Match
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(without alignments)
826:939 Million cell updates/sec
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AAD04761
AAD04738
ABL32074
AAD28364
AAA199905
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   6 Human alp
1 Human alp
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AAS73144
AAS73149
AAS75193
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AAQ29703

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AAD00296

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AAF317
Adb52677 Primary r
Aa292703 IRS-1. 3/
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Aa20296 Mouse ova
Aad00296 Mouse ova
Aad00297 Mouse ova
Aad18941 Human U62
Adb85264 Mouse RNA
Aaf2293 BAC conta
Aax18941 Human foe
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Aav89689 EST clone
Aac0230 Human foe
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Aai39774 Probe #75
Aba59131 Human for
Aak30771 Human for
Aak30771 Human pro
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Aak78536 Human imm
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Aak78537 Human GN
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Aas73114 DNA encod
Aas73119 DNA encod
Aas73110 DNA encod
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AAK22984 ABS48806 ABX90780 ABA62021 AAI41957 AAK36237

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ADC85287 ADA02807 ADB72545 ABQ88143 ABA74515 AAI54991 AAK49158

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Aai01628
Adc32621
Aas13648
Aaf16006
Aak52886
Aak51902
Adc31391
Abk84534
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8 Probe #16
1 Human nov
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6 Human pro
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        RESULT 2
AAI199906
ID AAI9
XX AAI9
AC AAI9
XX Huma
XX Huma
XX Huma
KW Poly
KW Cenit
KW Phos
XX Homc
XX Homc
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XX Homc
XX Key
FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC of a compound. The method comprises preparing a gene expression profile co of a tissue or cell sample exposed to the compound, and comparing the. CC gene expression profile to a database comprising SEO ID 1-4925, where cC differential expression of the gene indicates at least one toxic effect. CC of a compound, predicting hepatotoxicity or the progression of a toxic ceffect. CC of a compound, identifying an agent that modulates the onset or cC progression of a toxic response, predicting the ecllular pathways that a CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates the constitution using a database of genes having liver toxin-induced compositions of the colls for drug screening and toxicity markers in cC liver tissues or cells for drug screening and toxicity assays. Note: The specification, but was obtained in electronic format directly from WIPO cc at fftp.wipo.int/pub/published pct segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 51
                                                                         Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                               Human alpha-2BAR third intracellular loop variant encoding DNA
                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                          AAI99906;
                                                                                                                                                                                                                                                                                                                           AAI99906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 828 BP; 148 A; 271 C; 269 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002; 2
15-MAR-2002; 2
15-MAR-2002; 2
30-DEC-2002; 2
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; 2002US-0364045P;
; 2002US-0364055P;
; 2002US-0436643P;
Location/Qualifiers
1. .1344
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7.6e-05;
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ABV08936 AAF16382 AAS39178

ALIGNMENTS

AAS75454

AAF16006 AAK52886 AAK51902 ADE31391 ABK84534 ABN97204 ADB72389

118 119 120 121 123 123 124 125 126 127 128 129 130 131 133 134 135 136 137

AAKI 0337 AAB35921 AAD2859 ABT43583 ABT43583 ABT43586 ABT43586 ABT43586 ABT43586 ABT43586 ABT43586 ABC17326 ADC17326 ADA120916 AARIZ0916 AARIZ0917 AARIZ0066 AARIZ0916 AA

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RESULT 1
ADB59041
ID ADB5
XX
AC ADB5
XX
O4-I
XX
DE Toxi
XX
Toxi
KW Toxi
XX
CS Unic
Unidentified
                        Toxic; toxin; gene
                                       Toxicity-related gene, SEQ ID 4067.
                                                                04-DEC-2003
                                                                                  ADB59041;
                                                                                                  ADB59041 standard;
                screening;
                                                             (first entry)
        ene expression profile; hepatotoxicity; liver;
toxicity assay; ds.
                                                                                                 DNA;
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RESULT 3
AAD04761
ID AAD0
XX
AC AAD0
XX
                                                                                                                                                                                                                                                                                                  CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic cobtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A cor alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising; (a) comprising nucleotide positions 901-909 of (1), a site comprising (A) core alpha2C or fragment or complement of; and (b) detecting a polymorphic cytosine or guanine at position 901-909 of (1), a site comprising (A) core site comprising (A) core method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased crist of developing a disease associated with alpha2B, alpha2A or alpha2C, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. cpinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, cyrazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and comprisations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol complement of the human alpha-2BAR variant, the sequence is cof the wildtype gene (AAI39905)
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                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                         Matches
                  AAD04761
                                                AAD04761 standard;
                                                                                                                                                                                                                                                                            Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 144-145; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2000; 2000US-00551744
10-AUG-2000; 2000US-00636259
19-OCT-2000; 2000US-00692077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2001; 2001WO-US012575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-611728/70.
DB; AAM52118.
                                                                                                                                       880
                                                                                                                                                                                                           51;
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                                                                                                                                                                                                                             Similarity
                                                                                                                                                          GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCAG 51
                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG 930
                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Small KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "alpha-2BAR"
/note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909 of the
wildtype alpha-2BAR protein (AAI99905)"
                                                  DNA; 1344
                                                                                                                                                                                                           0,
                                                  ВP
                                                                                                                                                                                                         Score 51; DB
Pred. No. 7.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                         7.8e-05;
                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                         Length 1344;
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                                                                                                                                                                                                         0,
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RESULT 4
AAD44388
ID AAD4
XX

AAD44388

standard;

DNA;

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                                                                                                                    The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and capinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a chinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                       Best Loc
Matches
                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                    Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 24-26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            arteries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Snapir A,
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-2000; 2000WO-FI000913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200129082-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamic acid repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                 therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-300318/31.
DB; AAE00989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha2B-adrenoceptor (alpha2B-AR) variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
ic acid repeat; intracellular loop; chromosome 2; catechol
                                                        49;
                                                                        Similarity
                  GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGAGTGTGAACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heinonen P, A
M, Salonen JT,
, Kauhanen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00422985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1344
                                                                     93.7%;
96.1%;
                                                                                                                   A,
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I, Tuomainen T,
Valkonen V;
                                                                                                                    459
                                                       Score 47.8; D
Pred. No. 0.00
0; Mismatches
                                                        0
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                                                                                                                    400
                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karvonen M,
T, Lakka TA,
                                                                                                                    266 T; 0 U; 0 Other;
                                                     DB 5;
0.00057;
les 2;
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                                                                                   Length 1344;
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Nyyssoenen
                                                          Indels
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en K;
                                                        <u>,</u>
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930
                            51
                                                        Gaps
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AAD44388;

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RESULT 5
ABL32074
ID ABL3
XX ABL3
AC ABL3
XX ABL3
XX BL3
AC ABL3
XX U
DT 26-M
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
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KW anti
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Best Local S
Matches 49
         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                Human immune system associated gene SEQ ID
                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                    ABL32074 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 24-26; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a risk of hypertension and targeting treatment in a determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001FI-00000323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200266617-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domo sapiens
                                                                                                                                                                                                                                                                                                                                                                     980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-667063/71.
DB; AAE26633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                           ĠĀĠĠĀŢĠĀĀĠĊŢĠĀĀĠĀĠĠĀĠĠĀĀĠĠĀĠĠĀĠĠĀĠĠĀĠŢĠŢĠĀĀĊĊĊĊĀĠ
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                DNA; 6904 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 A; 459 C; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human alpha-2B-adrenoceptor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                93.7%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47.8;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
.00057;
es 2;
                                                                                                                                                    NO:
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                                                                                                                                                                                                                                                                                                                                             930
                                                                                                                                                                                                                                                                                                                                                                               51
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RESULT 6
AADZ8364
ID AADZ
XX AADZ
XX AADZ
XX AADZ
XX Huma
XX Huma
XX Huma
XX Beha
XX Homa
XX Homa
XX Deha
XX Deha
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Matches
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30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                            02-JUL-2001; 2001WO-EP007540
                                                                                                                                                          Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia; drug abuse; migraine; ds.
                                                                                                                  WO200202809-A2
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                         22-APR-2002
                                                                                                                                                                                                                                                                                                                                          AAD28364;
                                                                                                                                                                                                                                                                                                                                                                    AAD28364 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, arteriosclerosis, anaemia, cancer, acute myeloid rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6904 BP; 1244 A; 314 C; 2303 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 47; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurofibromatosis; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5880
                                                                                                                                                                                                                                                               chemically treated genomic DNA #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%;
95.6%;
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                                                                                                                                                                                                                                                                                                                                                                  6904
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Pred. No. 0.02:
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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PRRRX PXX PXX PTTTTTXX SXX XXX XXX XXX XXX
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Best Local S
Matches 43
17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder. Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA
                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                            central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; genBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                         Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
polymorphic site; allelic variant; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI99905 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-IC-receptor gene. The invention also relates to oligonuclectides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                              17-APR-2001;
                                                                                                                            WO200179561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 40-44; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5880
                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGATTGTGAA 5924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
 2000US-00551744.
2000US-00636259.
2000US-00692077.
                                                                2001WO-US012575
                                                                                                                                                             /*tag= a
/product= "alpha-2BAR"
/product= "sequence includes a 9 nucleotide polymorphic
/note= "sequence includes a 9 nucleotide polymorphic
at nucleotides 901-909 absent in the alpha-2BAR varis
(AAI99906)"
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          third
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ਨ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%;
95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ņ
                                                                                                                                                                                                                                                                                                                                                                                                                        intracellular loop encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ЧB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
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Gaps

0

site

Human 04-JUL-2001 AAD04762;

alpha2B-adrenoceptor (alpha2B-AR)

gene

(first

entry)

AAD04762 standard; DNA; 1353

BP.

0

norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.

Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol

catecholamine;

pectoris;

Cbs

Location/Qualifiers
1. .1353

sapiens

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AADO4762
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                                                                                                                                                                                                                                                                                          묽
                                                                                                                                                                                                                                                                                                                          The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) cobtaining a sample having a polymorlation so the comprising and polymorphic site, comprising; (a) cC or alpha-2B or fragment or complement of; and (b) detecting a polymorphic cities comprising nucleotide positions 901-909 of (I), a site comprising (A) CC cytosine or guanine at position 753 of (IIV) or a site comprising (A) CC (site comprising at positions 961-972 of (III)). The cytosine or guanine at position 753 of (IIV) or a site comprising (A) CC (site comprising at positions 961-972 of (III). The cytosine of further used for genotyping an alpha-2B, alpha-2A or alpha-2C receptor cytosine for general cytosine whether an individual is at increased crisk of developing a disease associated with alpha-2B, alpha-2A or alpha-2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict cytosinations of these. In addition, the technique may be used to predict cytosinations of these. In addition, the technique may be used to predict cytosinations, norepinephrine, clonidine, oxymetazoline, guanabenz, cymazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to phosphate levels). The present sequence is that of the third constitute a polymorphic site at nucleotides 901-019, absent in the alpha-2BAR (GenBank Accession AF009500), the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-019, absent in the alpha-2BAR (GenBank Accession AF009500).
                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                          Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 144; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphic site.
                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-611728/70
DB; AAM52117.
                                                                                                                 892 GAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                      44;
                                                                                                                                            4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGGETT
SMALL K
                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Small KM;
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                                                                                                                                                                                                                                                                                        224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                        81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                        Score 41.6;
Pred. No. 0.
                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                             4.
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                                                                                                                                                                                                                                               Length 1353;
                                                                                                                                                                                                      Indels
                                                                                                                 939
                                                                                                                                                         51
                                                                                                                                                                                                      0
                                                                                                                                                                                                      Gaps
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RESULT 9
AAD44389
ID AAD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element cacids (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Calpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-Catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-Catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-Catecholamines, norepinephrine and epinephrine suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries and a disease involving vascular coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as conficulally expressed as Prinzmetal's variant form or acute myocardial ax conficulation (AMI). Alpha2B-AR gene is used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 44
                                             W0200266617-A1
                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                   Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
                                                                                                                                                                                                                                                                                               Human alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                      AAD44389;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD44389 standard; DNA; 1353 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snapir A, H,
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 27-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300318/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salonen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-FI000913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200129082-A1
                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 91.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
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Salonen JT,
                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                 hypotensive; gene;
                                                                                 /product=
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00422985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%;
91.7%;
                                                         "Human alpha-28-adrenoceptor protein"
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T, Tuomainen T,
Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karvonen
T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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en K;
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RESULT 10
AAQ14:
JD AAQ14:
XX AAQ14:
XX AAQ14:
XX AAQ14:
XX AAQ14:
XX Human
XX Neuro
XX Homo
XX Homo
XX CDS
FT CDS
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FT CDS
FT CDS
XX PN US505.
XX O1-OC
XX O1-OC
XX O1-OC
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XX ON-O
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Best Local
                                 WPI; 1991-310087/42.
P-PSDB; AAR14149.
                                                                                                       Weinshank
                                                                                                                                                                                                                                   30,-OCT-1989;
                                                                                                                                        (NEUR-) NEUROGENETIC CORP
                                                                                                                                                                                             30-OCT-1989;
                                                                                                                                                                                                                                                                                 01-OCT-1991.
                                                                                                                                                                                                                                                                                                                              US5053337-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha 2 beta adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ14151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ14151 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1353 BP; 223 A; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-667063/71.
P-PSDB; AAE26634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001; 2001FI-00000323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 GÁAGAGGAGGÁÁGÁÁGÁÁGÁÁGÁÁGÁÁGÁÁGÁÁGTGTGÁÁÁCCCCÁG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                       RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                               Hartig
                                                                                                                                                                                   89US-00428856
                                                                                                                                                                                                                              89US-00428856
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
288. .1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002WO-FI000113.
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81.6%; 91.7%;

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Score 41.6; DB, Pred. No. 0.026; 0; Mismatches

6 4

Length 1353; Indels

51 0;

Gaps

0,

C; 405 G; 266 T; 0 U; 0 Other;

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2064

ВP

receptor gene.

Isolated DNA encoding

human

adrenergic receptor -

for detecting nucleic

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AAT59499
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bind to, th
                                       A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAW11804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and in the second control of the second cells are deposited as ATCC CRL 10275.
                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2A-E; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1989;
30-MAY-1991;
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06-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone NGC-alpha2beta was isolated from a human spleen genomic library screening with a fragment of the human 5-HTA receptor gene. The gene be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor function
                                                                                                                                                                                                                                                                                                                                                                                   Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hart1g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha-2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT59499
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91US-00707604
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                        receptor.
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Pred. No. 0.
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                                                                                                                                      CC polynuclectide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an CC array element in a microarray for monitoring the expression of a number CC of target polynucleotides. The microarray is particularly useful in the CC diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug CC discovery and development, toxicological and carcinogenicity studies, CC monitoring progression of diseases and for developing sophisticated CC profiles for the effects of currently available therapeutic drugs. The CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs CC array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose CC various diseases including cancer e.g. adenocarcinoma and leukaemia, disease of immunorathies are although as them a compression of a disease.
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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AlDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2064 BP;
                                                                    immunopathies e.g. AIDS and asthma, neuropathles e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microarray for mo
polynucleotides...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a combination which, comprises a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human signalling pathway polynucleotide probe SEQ ID
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                                   seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
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                                                      directly from USPTO
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91.7%;
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Pred. No. 0
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04-MAR-2003

(first entry)

ABZ42624 standard;

Query Match Best Local (

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Conservative

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The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC and (2) an isolated antibody having high specificity and high affinity or captidity for a particular GPCR. (I) can be used as GPCR modulators and in the polydespecial peptides for GPCR antibody against a particular GPCR. (I) can be used as GPCR modulators and in the polydespecial control of the specific captides for GPCRs and in the production of specific captides and antibodies are also useful in detecting an CC presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for detecting the CC treating immune-related diseases, growth-related diseases, cell used the second control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 523pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; halzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; mental retardation; epilepsy; asthma; tuberculosis; dementia; memory loss; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2001; 2001WO-US050107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 3274
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91.7%;
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.027;
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                                                                                  Sequence
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Matches 44
                                                                                                                                                                                                                                                                                                                                                            The present sequence is 3' end cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2G; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated DNA sequence encoding a melanoma tumor associated antigen, useful for detection, diagnosis and staging of melanomas, monitoring metastatic melanomas and as a target for immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-308473/32.
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(LIFE-) LIFESPAN BIOSCIENCES 19-DEC-2000; 2000US-0257144P

Roush CL,

08-AUG-2002 W0200261087-A2 Homo

P-PSDB; ABP81780.

Lobuglio

ĀΕ;

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Human; melanoma tumour-associated antigen; cytostatic; gene therapy; vaccine; cancer; immune response; metastatic melanoma; immunotherapy; ss
                                                      3' end of human melanoma tumour-associated antigen cDNA from
                                                                                                                                                                         AAD06932 standard; cDNA; 593
                                                                                                                                                                                                                                                                                                                                                                                                            anxiety, depression, schizophrenia, dementia, mental retardation, memo 1088, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABR82018, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                         4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;
                                                                                                         (first entry)
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91.7%;
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Pred. No. 0.02/
0; Mismatches
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                                                    clone 5.31.
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Matches
                                                                                                                                          tumour-associated antigen. The cDNA is useful in gene therapy and as an associated who is at risk of getting mRNA coding for the melanom individual who is at risk of getting cancer, suspected of having cancer or has cancer. The present sequence is useful for vaccinating an melanoma tumour by inducing an immune response against it. The melanoma inmunotherapy. The identification of the melanoma and staging metastatic melanoma, as new targets for recurrence and metastatic disease to be detected and disease burden of particular use in melanoma tumour associated antigen is useful for detection, diagnosis and staging recurrence and metastatic disease to be detected and disease burden of particular use in melanoma research
             Conservative
                                                                                                        158 A; 115
                               71.8%;
82.4%;
               0
                          Score 36.6;
Pred. No. 0.
                                                                                                      C; 146
                                                                                                   G; 174
                                            DB 4;
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9;
                                       Length 593;
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GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG

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The invention relates to novel purified or isolated nucleic acids of cessential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object characterisation or to prevent or inhibit formation on a surface of a comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and comparing oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an expension patterns, for raising anti-protein antibodies, as an confidence of a surface correlative receptors or to identify inhibitors of the binding cours or to identify inhibitors of the binding cours of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence contained to the essential contained to the invention of the essential contained to the invention of the essential contained to the invention of the invention
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 175pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus essential gene #2614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
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Sequence 2367 BP; 630 A; 644 C;

681 G;

412 T; 0 U; 0 Other

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CC organism such as A. timigatus, to treat a non-infectious disease in a CC subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a CC biofilm comprising A. fumigatus. The polynucleotides are useful for CC companisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify CC potential orthologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the binding CC interaction. The polypeptides may be used to raise antibodies or to clicit immune response, as a reagent in assays designed to quantitatively host tissues in which pathogenic organism livade or reside, and to constitute correlative receptors or ligands in the case or virulence
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Best Local
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05-JUN-2001;
09-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2003
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; 2001US-0295890P.
; 2001US-0303899P.
; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   essential gene; Aspergillus fumigatus; infection; biofilm: antibody; immune response; ds.
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Pred. No.
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RESULT 17
ABT1784
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The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus funigatus. The isolated nucleic acids of CC the invention are used to treat or prevent infections by a pathogenic CC organism such as A. fumigatus, to treat a non-infectious disease in a CC subject (e.g. cancer), to prevent or contain contamination of an object CC by A. fumigatus, or to prevent or inhibit formation on a surface of a CC by A. fumigatus. The polynucleotides are useful for CC contain comprising A. fumigatus. The polynucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC contains invade or reside, for comparing with the DNA sequence of A. CC contains invade or reside, for comparing with the DNA sequence of A. CC similar biochemical activity and/or function, for comparing with DNA CC contential orthologous essential or virulence genes having the same or sequences of other related or distant pathogenic organisms to identify CC making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an CC response, and for identifying polynucleotides encoding the other protein interaction. The polypeptides may be used to raise antibodies or to identify the binding occurs or to identify inhibitors of the binding country interaction. The polypeptides may be used to raise antibodies or to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
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genes of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGTGTGA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fumigatus essential gene #204.
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88.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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CC The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of CC the invention are used to treat or prevent infections by a pathogenic conganism such as A. fumigatus, to treat a non-infectious disease in a CC by A. fumigatus, to treat a non-infectious disease in a CC by A. fumigatus, to treat or contain contamination of an object confirm comprising A. fumigatus. The polynucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC indigatus to identify duplicated genes in which the pathogenic CC fumigatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with the DNA sequence of A. CC sequences of other related or distant pathogenic corganisms to identify and/or function, for comparing with DNA cC sequences of other related or distant pathogenic organisms to identify and/or function and organisms to identify corganisms to identify corganisms to identify and/or function organisms to identify and corporate or attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                              Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                 New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus essential gene #2018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABT19660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polynucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGAGAGTGTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eroshkin AM,
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Best Local S
Matches 39
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
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23-MAR-1999
06-APR-1999
06-APR-1999
16-APR-1999
16-APR-1999
23-APR-1999
24-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polynucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybridisation assay; genetic mapping; gene eprotein identification; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.6%;
nilarity 88.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana DNA fragment
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                                                                                                                                                                                                                                                                                                                                                                                             2000EP-00301439
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99US-0121825P
99US-0123548P
99US-0125788P
99US-0126764P
99US-0126785P
99US-0126785P
99US-0126785P
99US-0130677P
99US-0130677P
99US-0130649P
99US-0132485P
99US-0134256P
99US-013421P
99US-0134758P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence; ss.
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Pred. No. 0.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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pathway; metabolic pathway;
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18-JUN
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21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
27-MAY-1999
28-MAY-1999
01-JUN-1999
03-JUN-1999
04-JUN-1999
07-JUN-1999
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99US-0115124P

99US-013523P

99US-013623PP

99US-0136732PP

99US-0137522PP

99US-0137522PP

99US-0137522PP

99US-0138647PP

99US-0139453PP

99US-0139453PP

99US-0139454PP

99US-0149484PP

99US-0149484PP

99US-0149484PP

99US-014928PP

99US-014928PP

99US-014928PP

99US-0149334PP

99US-014934PP

99US-014934PP

99US-014934PP

99US-014508PP

99US-014508PP

99US-014518PP

99US-0145218PP

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Query Match
Best Local Similarity
Matches 38; Conserve
                                                               RESULT 20
AAQ88817
ID AAQ88
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                                                          Porcine and human SPAR cDNAs were compared. They are highly homologous, divergent. The 32.3 kDa human and 32.8 kDa porcine ORFs are show structural features consistent with cell membrane-bound receptors. Porcine counterpart. The pspar protein is predicted to that of its a secondary structure of hspar ORF is similar to that of its porcine counterpart. The pSPAR protein is predicted to have a hydrophoic a second alpha helix of 28 residues beginning at AA 48. It is followed by a turn, pleated sheets. Human SPAR ORF has a 25 AA hydrophobic alpha-helix near a second alpha helix of 24 residues then a series of turns and betastring at residue 29, followed by beta-pleated sheets and turns. Another 28 residue beta- helix begins near AA 200. (Updated on 25-MAR-2003 to correct PN field.)
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PR
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PR
                                               Sequence 1820 BP; 501 A; 393 C; 418 G; 508 T;
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Best Local S
Matches 38
                                                                                                                                                                                                                                           Compsn. capable of binding to surfactant protein-A receptor - which modulates secretion of alveolar surfactant, e.g. to treat respiratory
                                                                                                                                                                                                                    Disclosure; Page 35-36; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                              WPI; 1995-115402/15.
P-PSDB; AAR71460.
                                                                                                                                                                                                                                                                                                                               Strayer DS,
                                                                                                                                                                                                                                                                                                                                               (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1994;
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09-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAR; surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human surfactant protein A receptor (hSPAR) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ88817 standard; cDNA; 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L Similarity 88.4
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                     93US-00114951.
93US-00176218.
                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US009752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
                  68.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%;
    ; Score 35; DB 2
; Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A receptor; respiratory distress syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽₽
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                           2
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   5; Indels
                                             0 U; 0 Other;
                      Length 1820;
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 0;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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10-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999; 20-SEP-1999;

01-SEP-1999; 07-SEP-1999;

16-AUG-1999 17-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 26-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 27-AUG-1999 31-AUG-1999 31-AUG-1999 31-AUG-1999

99US-014684P 99US-014936P 99US-014917SP 99US-0149426P 99US-0149723P 99US-0149723P 99US-0149920P 99US-0149930P 99US-015084P 99US-015106P 99US-015106P 99US-0151000P 99US-0151303P 99US-0151303P 99US-01513363P

09-AUG-1999; 09-AUG-1999; 10-AUG-1999;

99US-0147038P 99US-0147302P 99US-0147302P 99US-0147302P 99US-0147303P 99US-0147303P 99US-0147416P 99US-014793P 99US-014793P 99US-0148171P 99US-0148171P 99US-0148141P 99US-0148341P 99US-0148341P

02-AUG-1999, 02-AUG-1999, 02-AUG-1999, 03-AUG-1999, 03-AUG-1999, 04-AUG-1999, 04-AUG-1999, 05-AUG-1999, 06-AUG-1999, 06-AUG-1999,

99US-0146386P. 99US-0146388P. 99US-0146389P. 99US-0147038P.

22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 28-SEP-1999; 29-SEP-1999;

04-OCT-1999 05-OCT-1999 06-OCT-1999 07-OCT-1999 08-OCT-1999 12-OCT-1999 13-OCT-1999 13-OCT-1999

99US-0153070P 99US-0154018P 99US-015403P 99US-0155436P 99US-0155436P 99US-0155436P 99US-015556P 99US-015717P 99US-015717P 99US-0158029P 99US-0158029P 99US-0158232P 99US-015923P 99US-015923P 99US-015923P 99US-015923P 99US-015923P 99US-015923P 99US-015923P 99US-015933P 99US-015933P 99US-015933P 99US-01693P 99US-016076P 99US-0160815P 99US-0160981P 99US-0160981P 99US-0161404P 99US-0161408P 99US-0161408P

14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 21-OCT-1999 21-OCT-1999

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1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTG 43

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CC designated ORF (open reading frame) 1-4334, and sequences ABN75054-CC ABN75897 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively CC referred to as ORFX) proteins, polynucleotides at least 85% identical to CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and CC polypeptides, methods of screening for modulators of ORFX expression or CC activity, and methods of screening individuals for a predisposition to an CC orex-associated disorder. The ORFX proteins of the invention have a wide crange of biological activities, such as cytokine, cell proliferation, CC clisue growth, angiogenesis, activitor, haematopoiesis regulation, creceptor/ligand, antiinflammatory activity, thrombolytic activity, cand mitinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, cultivated as and antibodies may be used in the treatment of cancers, cother proliferative disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1036; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2001; 2001WO-US017076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidsm; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis repartation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cransplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106200/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2000; 2000US-0206690P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORF1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN76609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN76609 standard; cDNA; 392 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABP32583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:3111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614
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RESULT 22
AAV25477
ID AAV25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage diseases, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases
Sequence 5000 BP; 1238 A; 1287 C; 1243 G;
                                       The present sequence encodes a new sulphonylurea receptor (SUR2) protein isolated from a rat brain cDNA library. The sequence can be derived from animals such as human or rat. Products of SUR2 can be used for diagnosis and treatment of potassium channel diseases, e.g. hypertension and
                                                                                                                                       New sulphonyl-urea receptor protein - useful treatment of potassium channel diseases such
                                                                                                                                                                                  P-PSDB;
                                                                                                              Claim
                                                                                                                                                                                                WPI; 1998-200632/18.
                                                                                                                                                                                                                            (NICH-)
                                                                                                                                                                                                                                                                      09-AUG-1996;
                                                                                                                                                                                                                                                                                                 09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                        JP10052275-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potassium channel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; sulphonylurea receptor; SUR2; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat sulphonylurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV25477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV25477 standard; cDNA; 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 392
                                                                                                              2; Fig 7-11;
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                                                                                                                                                                                                                           KIYONO
JAPAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGTGTGA 44
                                                                                                                                                                                   AAW53602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGATGAGGAAGAAGAGGAGGAGGAAGGAAGAGGGAAGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 116 A; 64 C; 112 G; 100 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                            CHEM RES
                                                                                                                                                                                                                                                                      96JP-00227552
                                                                                                                                                                                                                                                                                                96JP-00227552
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
271. .4908
                                                                                                                                                                                                                                                                                                                                                                                              /product= "SUR2"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "sulphonylurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor SUR2 encoding cDNA.
                                                                                                              19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%;
                                                                                                                                                                                                                            8
                                                                                                              Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
1232 T; 0 U; 0 Other
                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                       for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                          ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 392;
                                                                                                                                                       e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                      diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholesterol ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Query Match

67.5%;

Score 34.4;

DB

'n

Length 5000;

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ABSULT 23
ABT4189
ID ABT4189
ID TAXX
AST4189
AST411
AC ABT411
AC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the renal toxic of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-2001; 2001US-0292335P.
13-JUN-2001; 2001US-029925P.
19-JUN-2001; 2001US-0303800P.
10-JUL-2001; 2001US-0303800P.
10-JUL-2001; 2001US-0303810P.
10-JUL-2001; 2001US-0315047P.
27-SEP-2001; 2001US-0315047P.
27-SEP-2001; 2001US-031462P.
01-NOV-2001; 2001US-0330462P.
01-NOV-2001; 2001US-0330467P.
06-DEC-2001; 2001US-03316344P.
19-DEC-2001; 2001US-0336144P.
19-EEB-2002; 2002US-0357843P.
21-FEB-2002; 2002US-0357843P.
21-FEB-2002; 2002US-0357843P.
21-FEB-2002; 2002US-0357844P.
15-MAR-2002; 2002US-0357843P.
15-MAR-2002; 2002US-0357843P.
15-MAR-2002; 2002US-0370244P.
08-APR-2002; 2002US-0370244P.
                                                                                                                                                                                                                                   Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Predicting
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-148464/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200295000-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               database;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxicity modelling
                                                                                                                                                                                                                                                                                  reast l sample exposed t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABT41889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  effect; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE
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                                                                                                                                                                                                                                                                                                                                                                   at least
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0371679P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002WO-US016173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening;
                                                                                                                                                                                                                                                                                  one toxic effect of a compound, useful for toxicity preparing a gene expression profile of a tissue or to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression profile; renal toxicity; toxicity marker; eening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.48;
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RESULT 24
ADBS8175
ADBS8175
AND ADBS8175
AXX ADBS88
AXX ADBS8
AXX ADBS8
AXX Toxic
AXX IS-MA
AXX 
CC The present invention relates to a method for predicting a toxic effect CC of a compound. The method comprises preparing a gene expression profile conference of the sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC differential expression of the gene indicates at least one toxic effect. CC compound, predicting hepatotoxicity at least one toxic effect of a CC of a compound, identifying an agent that modulates the onset or CC compound modulates in a cell, and identifying an agent that modulates the onset or CC compound modulates in a cell, and identifying an agent that modulates the cellular pathways that a CC least one activity of a protein. The method and compositions of the CC differential expression, are useful in identifying toxicity markers in the rissues or cells for drug screening and toxicity assays. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3201; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises preparing gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Predicting a toxic effect markers in liver tissues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002; 2002US-00060087.
15-MAR-2002; 2002US-0364045p.
15-MAR-2002; 2002US-0364055p.
30-DEC-2002; 2002US-0436643p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxicity-related gene, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB58175 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in menitoring disease physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this pate did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5000 BP; 1238 A; 1284 C; 1246 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porter M,
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86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t of a compound, useful in identifying toxicity or cells for drug screening and toxicity assays, expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6628
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Pred. No. 2.4;
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RESULT 25
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19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002;
13-MAR-2002;
08-APR-2002;
                                                                                                                                        Mendrick
Elashoff
The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to
                                                                       Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express profile of a tissue or cell sample to a database of Tox mean and non-
                                                                                                                                                                                                                                                                                          10-APR-2002; 2002US-0371150P.
11-APR-2002; 2002US-0371413P.
19-APR-2002; 2002US-0373601P.
19-APR-2002; 2002US-0373602P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxic effect; gene expression profile; toxicity marker; toxicity progression; primary rat hepatocyte toxicity modelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primary rat hepatocyte toxicity modelling
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                                           SEQ
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2002US-0378653P.
2002US-0378665P.
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2002US-0378370P.
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2003US-0442900P
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2002US-0394253P.
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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for
                                                                                                                             Purified nucleic acid encoding Insulin Receptor Substrate - us prepare IRS-1, for diagnosis and treatment of insulin related and abnormal cellular proliferation.
                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                  Kahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
17-MAR-1993
                                                                                                      Disclosure; Fig 12;
                                                                                                                                                                                                                                                                                        17-JAN-1992;
                                                                                                                                                                                                                                                                                                              06-AUG-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxicity modelling related gene sequence from the present
                                                                                                                                                                                                                                                                18-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                               rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor substrate-1; IRS-1; probe; vector; etabolism; insulin related disease; ss.
                                                                                                                                                                              AAR28047.
                                                                                                                                                                                                                                        JOSLIN
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(first en
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                                                                                                                                                                                                                                        DIABETES CENT INC.
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                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 589. .2053 /*tag= a
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                                                                                                       128pp; English.
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86.4%;
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ed diseases
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The sequence given encodes the rat insulin receptor substrate-1 (IRS-1). The IRS-1 was isolated using the probe sequences given in AAQ29701-02. The IRS-1 sequence can be inserted into a vector and used to transform cells to produce IRS-1. The level of IRS-1 metabolism can then be studied and abnormal levels may be seen to be indicative of insulin related disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence

5125

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0 Other

Best Local Similarity

66.3**%;** 84.4**%**;

Score 33.8; Pred. No. 3;

ĎΒ 5 u;

0 Other;

Query Match

Sequence 291

₽₽;

129 A; 22 C; 112 G; 28 T; 0

ftp.wipo.int/pub/published\_pct\_sequences

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sequences. (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polymucleotides are also used (CC genes. (I) is useful in gene therapy techniques to restore mapping, CC genes. (I) is useful in gene therapy techniques to restore mapping, CC genes. (I) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore mormal (CC useful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food (CC state of the sypressing (II). (I) and (II) are useful for treating disorders (CC supplement. (II) and its binding partners are useful in medical imaging (CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations (CC diagnostics, forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and (CC coding sequences AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPD (CC electronic format directly from WIPD (CC) and to int/muh/muhlished for this content in the printed specification, but was obtained in CC electronic format directly from WIPD (CC) and to the present in the printed specification of the content of this content of the product of the content of the conte
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4730; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #4730.
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)B; ABG04739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
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83.0%;
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The present sequence is that of murine ovary-specific O1-236 cDNA. O1-236 CC is the mammalian orthologue of xenopus laevis nucleoplasmin, and the O1-CC 236 gene has been named Npm2 (see also ABZ24594). O1-236 clones were CC initially identified by subtractive hybridisation using ovaries from Gdf9 CC knockout and wild-type mice. Full-length Npm2 cDNA (clone 236-1) was used CC chromosome 14. Loss of Npm2 gene in a genomic library. This gene maps to CC chromosome 14. Loss of Npm2 results in female infertility and converted to the invention provides ovary-specific and occyte-specific CC golypeptides. These genes and their protein products appear to relate to involving ovarian tumours, such as germ line tumours and granulosa cell provides a method for detection of a cell proliferative or degenerative ovarian failure. The invention CC ol-184 or O1-236. It also provides a method for treating such disorders of the ovary, which is associated with the expression of O1-180, O1-184 or O1-236, and a method of screening for compounds that gene a method of screening for compounds that genes. These compounds are possible contraceptive or fertility enhancing cc polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ24593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 111-112; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New ovary-specific-genes comprising O1-180 or O1-236, useful for decreasing conception or enhancing fertility, or for the preparation composition for treating e.g. cancer.
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Best Local S
Matches 38
                                                                             The present sequence is the mouse oocyte-specific gene Npm2, complete CDNA clone O1-236. It is derived from mouse 2-cell embryo cDNA library and expressed in the oocytes of intermediate size type 3a follicles and all type 3b follicles. This clone is used to screen and identify the mouse Npm2 gene. It is homologous to Xenopus laevis nucleoplasmin (Xnpm2) expressed exclusively in eggs. It provides in vitro and in vivo reagents for studying ovarian development and function. This sequence has gynaecological and contraceptive activity. Agents which modulate O1-180, O1-184 and O1-236 may be used to treat cell proliferative or degenerative genes. This ovary-specific sequence can be used as reagents to evaluate potential contraceptives, to block ovulation in a reversible manner. It is also used to screen for genetic mutations in signalling pathways, that are associated with some forms of human infertility or gynaecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01\text{-}180, 01\text{-}184 and 01\text{-}236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner.
  Sequence 1019 BP; 334 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Fig 5; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang P;
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/product= "Mouse occyte-specific protein, 01-236"
/note= "Identical to mouse Npm2 protein with the
exception of one residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.3%;
84.4%;
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  243
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Pred. No. 3.
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  U; 0 Other
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Best Local S
Matches 38
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/*tag= j

/note= "The '

512. .542

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527
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/*tag= g
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672
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/*tag= c
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657. .687
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543. .656
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/note= "Corresponds
....an bases 526 an
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/number= 3
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151. .199
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/note= "Corresponds to 105 missing nucleotides of intron
2 between bases 409 and 411"
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/product=
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337. .1177
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/note= "Corresponds to 314 missing nucleotides of intron
/ between bases 214 and 216"
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oding region is interrupted by 8 introns"
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Pred. No. 3.2;
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misc\_feature

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01-180, 01-184 and 01-236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner.
                                   WPI; 2000-350684/30.
P-PSDB; AAY70951.
                                                       Matzuk MM, Wang P;
                                                                                       28-OCT-1998;
                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                      28-OCT-1999;
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/note= "The
1361. .1366
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/*tag= z
/number= 8
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/note= "Corresponds to 63 missing nucleotides of intron
Detween bases 1116 and 1118"
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/note= "Corresponds to 471 missing nucleotides of intron
/ between bases 1051 and 1053"
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1037. .1067
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/number= 7
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/*tag= t
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/note= "Corresponds to 157 missing nucleotides of intron
5 between bases 979 and 981"
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/*tag= q
/number= 5
797
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/note= "Corresponds to 1321 (1.32kb) missing nucleotides
of intron 5 between bases 796 and 798"
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/*tag= o
/note= "Corresponds to 2771 (2.77kb) missing nucleotides
of intron 4 between bases 671 and 673"
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Search completed: February 29, 2004, 20:36:16
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                                                                                                                                                                                                                             CC The present sequence is the mouse ovary-specific Npm2 gene, mapped to the middle of mouse chromosome 14. It shows linkage to D14Mit32, this region cc being syntenic to human chromosome 8p21. The clone 01-236 cDNA is used to screen and identify Npm2 gene. It is the mammalian ortholog of xenopus clavis nucleoplasmin (Xnpm2) expressed exclusively in the eggs. It cc and function. This sequence has gynaecological and contraceptive activity. Agents which modulate 01-180, 01-184 and 01-236 may be used to treat cell proliferative or degenerative disorders, associated with cc admormal expression of these ovary specific genes. This ovary-specific contractions in a reversible manner. It is also used to screen for cc generic mutations in signalling pathways, that is associated with some xx form of human infertility or gynaecological cancer
                                                                                                                                                        Query Match
Best Local S
Matches 38
                                                                                                                                                                                                     Sequence 1481 BP; 407 A; 379 C; 391 G; 296 T; 0 U; 8 Other;
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Local L
38;
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                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
                                                                                                                                              Similarity 84.4%;
Similarity 84.4%;
38; Conservative
                                                        ĠĀĀĠĀŤĠĀĊĠĀĠĠĀĀĠĀĠĠĀĠĠĀĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀŢĠĀĀ 877
                                                                                                                                    Score 33.8; DB Pred. No. 3.3; 0; Mismatches
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Listing first 150 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 1044)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                            892
                                                                                                                  AGENCOURT 8113358 Lupski_dorsal_root_ganglion Homo sapiens cDNA 6880026 RANA Sequence.

BQ880026 RANA sequence.

BQ880026.1 GI:22272034
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Similarity 91.7%;
44; Conservative (
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1353)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,B.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1353)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963 (2003)
14671302
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AY416856.1 GI:39772816
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                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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<1. >1353
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Indels Length 1353;

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EST 16-AUG-2002

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                                                                                                   2 (bases 1 to 1347)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                           Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
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AY416858
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                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                              Inferring nonneutral evolution from human-chimp-mouse orthologous
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High quality sequence stop: 430.
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                   sequence was made by sequencing based on alignment.
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/clone lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGACCGGCCCCT(15)-3'. Size selected
1'kb for average insert length 1.7 kb. This is a primary
1ibrary, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo
College of Medicine) and is available through Life
Location/Qualifiers
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
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Xenopodinae; Silurana.

1 (bases 1 to 633)

1 (croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Roge Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

On Sep 15, 2002 this sequence version replaced gi:22893073

Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                            43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGAGTGTGAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                        Silurana tropicalis (western clawed frog) Silurana tropicalis
                                                                                                                                                                                            AL872808 XGC-egg Silurana tropicalis cDNA
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-SEP-2001) MRC Centre Hinxton, Cambridge, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hunter, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 872)
Hunter,C. and Elgar,G.
Alpha2 adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; Alpha2 adrenergic
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                                                                                                                                                                 AL872808.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                        GAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAGCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DN
/db_xref="taxon:9796"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Equus caballus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                 GI:38666205
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86.0%;
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Pred. No. 55;
0; Mismatches
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Pred. No. 43;
O; Mismatches
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CB10 1SB. UK Email:
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                                                                                                                                                                                                      ar EST 03-DEC-2003
TEgg106k18 5', mRNA
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                                                       and Rogers, J
                                                                                              Euteleostomi;
; Pipidae;
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Query Match
                                                          Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEGG9015d14.plkSP6
TROPICALIS_SEQUENCE ID: TEGG9015d14.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) lib:
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) lib:
CONSTRUCTED by Aaron M. Zorn.
CDNA was oligo dT primed from 5ug of poly A+ RNA from egg
Sound and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site_2: NotI
Host: Eschericha coli XII-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 GTGGÁTGAÁGATGAÁGAGGÁAGATGÁGGÁTGÁGGÁGTGTGAÁCCAC 511
                                                                                                                                                                                                                                                                                                                                                                                   Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. a Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                 On Sep 15, 2002 this sequence version replaced gi:22872961
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis (western clawed frog) Silurana tropicalis
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AL852740 XGC-egg Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TROPICALIS_SEQUENCE ID: TEGG106k18.plkSp6
Sequencing primer: $\frac{7}{8}6$
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

CONA was oligo dT primed from Sug of poly A+ RNA from egg.

ECORI-Not1 cut cDNA was then ligated into pCS107 with EcoRI at 'end and Not1 at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site_2: Not1

Host: Escherichia coli XLI-blue.
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Hinxton, Cambridgeshire, CB10 157, ...
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus TS SEQUENCE ID: TEGG106k18.plkSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 634)
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/organism="Silurana tropicalis"
/mol_type="mRNA"
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="egg"
/lab host="Escherichia coli XL1-blue"
/lab host="Escherichia coli XL1-blue"
/clome libe="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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xref="taxon:8364"
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85.7%; Pred. No. 64;
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is cDNA clone TEgg015d14 5', mRNA
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                                                                                                                      egg.
EcoRI at the
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CF360731/c
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REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

RESULT 6 AL852740/c

DEFINITION

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ORIGIN

Local

FEATURES

source

COMMENT

TITLE JOURNAL

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RESULT 8
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Best Local :
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                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: SRG8014 row: O column: 4 Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: SRG8014 row: O column: 4
                                                 GAĞGAGĞAAĞATGAAĞAĞĞAĞĞAAĞAĞĞAAĞAAĞAAĞAĞTĞAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 642) Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nomeman, D.J., Wray, J.E. and Keele, J.W. A second set of porcine ESTs from a pooled-tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (pig)
Sus scrofa
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.1%; Score 37.8; ilarity 85.7%; Pred. No. 64; Conservative 0; Mismatches
                                                                                                                                                                                                              /clone_lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled From multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                         organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:8364"
/clone="TBgg015d14"
/dev stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cD was oligo dr primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                72.5%;
88.9%;
                                                                                                                             Score 37; DB:
Pred. No. 96;
0; Mismatches
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                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                         BZ195097
CH230-248P14.TV CHORI-230 Segment 2 Rattus CH230-248P14, genomic survey sequence.
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,P., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
Other_ESTs: CH3#019_B01T3
                                                                                                                                                                                                                     BZ195097.1 GI:23853149
                                                                                                                                                                                                                                     BZ195097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: al.george@vanderbilt.edu
Insert Length: 1072 Std Error: 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 615 936 2660
Fax: 615 936 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vanderbilt University
529 Light Hall, 2215 Garland Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris
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BU748295.1 GI:23700479
EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: George AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags from Canine heart 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                   Kattus
                                                                                                                                                                            Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                              GATGAAGAAGCAGAAGAGGAGGAGGAGGAGGAAGAGGATGAA 85
                                                                           (bases 1 to 770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 787)
Y., Desai,R., Ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence start: 41 quality sequence stop: 785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: heart; Vector: pBluescript; Site_1: 5' of vector NotI; Site_2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo-dT primed"
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cell_type="heart"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage="mixed developmental stages (adult, 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="CH3#019_B01"
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88.9%;
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  Library CHORI-230 MboI segment
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                                    Geer,K.,
Russell,D., Chen,D.,
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Canis.
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                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                   sequence:
82-200, >(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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page: http://www.tigr.org/tdb/bac_end8/rat/bac_end_intro.html
plate: 248 row: P column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: CH230-248P14.TJ
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA315228.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE:6809872 5',
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                                                                          The following repetitive elements were found in this cDNA requence: 37-156, >(GGA)n#Simple_repeat (matched complimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s clone was contributed by the Brain Molecular Anatomy Project
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    e: 37-156, >(GGA)n#Simple_repeat (matched compliment)
    >(GAA)n#Simple_repeat (matched compliment)
    #Simple_repeat (matched compliment)

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/clone_lib="CHORI-230 Segment 2"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: Mb
/note="Vector: pTARBAC1.3; Site 2: Mb
/note="Textor: pTARBAC1.3; Site 2: Mb
/note="Te
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/clone="CH230-248P14"
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/strain="BN/SsNHsd/MCW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:24533352
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Pred. No. 1.3e+02; 
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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FEATURES

Seq

primer: pyx-5

/strain="C57BL/6" /organism="Mus musculus" ocation/Qualifiers

/mol\_type="mRNA" /db\_xref="taxon:10090" /clone="IMAGE:1295340" /organism="Mus musculus

```
Contact: Marra M/Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. La Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                       Fax: 314 200 101V
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ,
info@image.llnl.gov) for further i
                                                                                                                   Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence ston. 340
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 490)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Waterston, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA896321 . 490 bp mRNA linear EST 06-APR-1990 clone IMAGE:1295340 5, similar to gb:X56135 Mouse mRNA for AA896321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA896321.1 GI:3032714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole brain"
/dev_stages_embbryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T] phage resistant)"
/clone_ilb="NHH BMAp FWO"
/clone_ilb= Rccrition_ilb= Rccr
                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:10090"
'clone="IMAGE:6809872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.0%;
83.7%;
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Pred. No. 1.3e
0; Mismatches
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8;
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                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
       Query Match
Best Local Similarity
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VERSION
KEYWORDS
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AUTHORS
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ORGANISM
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CB625989
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                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                Seq primer: gta aaa cga cgg cca gtg.
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BACKWARD: gga aac agc tat gac cat
Plate: 15 row: O column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Ekkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB625989 mRNA linear EST 08
OSIIEa15013.f OSIIEa Oryza sativa (indica cultivar-group)
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CB625989.1 GI:29620978
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                                                                                        /clone="OSIIRALSO[3"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIRA"
/note="Vector: pBluescript I.
XhoI; Lesion Mimic_SPL_11"
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                                                                                                                                                                                                                                                                          /organism="Oryza sativa (indica cultivar-group)"
|mol_type="mRNA"
|cultivar="IR36"
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88.6%;
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  Score 36;
Pred. No.
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Pred. No. 1.5e+02;
Mismatches 5;
; DB 14;
1.6e+02;
                                                                                                                II KS
                                                                                              +; Site_1: EcoRI; Site_2:
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RESULT 11 AA896321

Snoor

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65

ORIGIN

Query Match Best Local Matches

EST 08-APR-2003

0,

Gaps

0,

REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

COMMENT

TITLE JOURNAL

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RESULT 13
CB625990/c
LOCUS
SOURCE
ORGANISM
                                                                                                                   RESULT 14
BM659898/c
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                                                                                                                                                                                 594
BJP602768646.R1 CSEQFXL38 p
CDNA, mRNA sequence.
BM659898.1 GI:18962904
EST.
Sus scrofa (pig)
Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 822)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: gta asa cga cgg cca gtg
BACKWARD: gga asc agc tat gac cat g
Plate: 15 row: O column: 13
Seq primer: gga asc agc tat gac cat g.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between rice and Magnaporthe grisea Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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                                                                                                       BM659898
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                                                                                                                                                                                                                                                                                                                /clone lib="OSIIEa"
/note="Vector: pBluescript
XhoI; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:39946"
/clone="OSIIEa15013"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
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                                                                                                                                                                                                                                                      70.6%;
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Pred.
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                                                                                       pig
                                                                                                                                                                                                                                                         36;
                                                                                       bp mRNA linear EST 27-FEB-2002 thyroid and parathyroid Sus scrofa
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1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Neoptera; Orthopteroidea; Dictyoptera; Bla Blattidae; Periplaneta.

1 (bases 1 to 378)
Zhou,Z.W., Liu,Z.G. and Gao,B.
The construction of Periplaneta americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                     Immnology Department
Jiang Xi Medical College
106, Bayi Street, Nanchang, Jiangxi,
Tel: 86-0791-6363001
                                                                                                                                                                                                                                                                                                                                                                         lgG4 immunology screen 
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pa002 Periplaneta americana Lambda Express library Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: david.adelson@tamu.edu.
Location/Qualifiers
                                                                                                                                                                                                                                             Email: Zhouzhenwen28@hotmail
                                                                                                                                                                                                                                                                                                                                                        Contact: Zhou, Z.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplaneta americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplaneta americana (American cockroach)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="CSRQFXL38 pig thyroid and parathyroid"
/note="Organ: thyroid and parathyroid gland; Vector:
pBluescript SK+, Site 1: Not1; Site 2: EcoRI; sequence 5
of the insert (5'-NNN' ... NNNinsert)
of GGAANTTGAAGCTCCACGCGGTGGCGGCGCTCGAG. Sequence 3' of
the insert (AAGAATTGAATTCAAGCTTATCGATATCGATCACGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
/clone lib="Periplaneta americana Lambda Express library"
/note="Vector: Lambda Excell; These sequences were
screened by cockroach sensitive patients' IgG4 serum "
                                                              /tissue_type="whole body"
/dev_stage="nymph"
/lab_host="E.coli NM522"
                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:6978"
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/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                              clone="5"
                                                                                                                                                                                     organism="Periplaneta americana"
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Pred. No. 2e+02;
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Dictyoptera; Blattaria; Blattoidea;
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Best Local Similarity
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                              sequence.
BI961033
                                               81961033 446 B
MONO1_5_C04.b1_A005 Monocytes
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               BI961033.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vandenplas,M.L., Cordonnier-Pratt,M.-M., Sudman,M.L., Gingle, A.R., Pratt,L.H. and Moore,J.N. An EST database from equine (Equus caballus) monocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 k
MONO1_5 C04.91_A005 Monocytes
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B1961415
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(bases 1 to 399)
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                                                                                                                                                                                                                                                                           /organism="Equus caballus"
/mol_type="maNA"
/db_xref="taxon:9796"
/db_xref="taxon:9796"
/ceIl_type="Isolated peripheral blood monocytes stimulated vih E. coli lipopolysaccharide"
/clone_lib="Monocytes (MONOI)"
/note="Vector: pBluescript SK(-) from Lambda ZapII;
Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision."
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           GI:16319236
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86.7%;
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86.7%;
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Pred. No. 2e+02;
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Pred. No. 2e+02;
                                               446 bp mRNA linear 1
Ytes (MONO1) Equus caballus
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                                                               MRC Human Genome Mapping Project
Hinxton, Cambridge, CB10 1SB, UX
Email: biohelp@hgmp.mrc.ac.uk
Vector: pME18S-FL3
                                                                                                                                         Takifugu rubripes ESTs
Unpublished (2002)
Contact: Clark MS
                                      V_type: phagemid
PRIMER: ME-735FW
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Takifugu.
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AL842491
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Takifugu rubripes
ibrary created by umio Sugano
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Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence :
20. Three-prime sequences, which are obtained with PolyTMix or Tree gruencing primer, are presented as the reverse complement.
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The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vandenplas,M.L., Cordonnier-Pratt,M.-M. Gingle,A.R., Pratt,L.H. and Moore,J.N. An EST database from equine (Equus cab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Equus caballus"
/mol_type="mRNA"
/db_xref="taxon:9796"
/db_xref="taxon:9796"
/cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"
/clone_lib="Monocytes (MONOL)"
/note="Westor: pBluescript SK(-) from Lambda ZapII;
Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the Cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.4%;
86.7%;
             Koichi Kawakami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cordonnier-Pratt, M.-M., Sudman, M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.4; DB:
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                447 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Equus caballus)
                                                                                                                      Resource
         Masahide Sasaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                     linear EST 30-JUL-2002
e F000H05aE11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lant Biology
GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446;
     Yutaka Suzuki,
                                                                                                                                                                                                                                                           Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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AW760336
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This Clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1134 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Marrin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterstton, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW760336
496 bp mRNA linear EST 03-DEC-2001 8149a06.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-4619 5' similar to TR:082214 082214 T29E15.4 PROTEIN.;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Bunkyo-ku, Tokyo 108-8639, Japan Library sequenced by Melody S. Clark and Amanda Thompson MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; rosida; eurosida I; Fabalea; Fabaceae; Papilionoldeae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW760336
AW760336.1 GI:7692223
EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kiyoshi Kikuchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.SB. UK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 496)
                                                                                                                                         quality sequence stop: 424.
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pME18S-FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="adult"
clone_lib="F000H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:31033"
/clone="F000H05aE11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Takifugu rubripes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _type="mRNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shugo Watabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.4; DB Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Length 447;
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KEYWORDS
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CB272922/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 GAGGATGAGGATGATGAGGAGGAGGAGGAGGATGTGTNTGACC 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 bp mRNA linear E mai64d07.yl McCarrey Eddy spermatocytes Mus musculus IMAGE:6446341 5', mRNA sequence.
                                                                                                                                                                                                                             1 (bases 1 to 512)
MCCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
Bennett,J., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAAC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
Tel: 314 286 1800
Fax: 314 286 1810
                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                   NIEHS Mouse
                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                      NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                             Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB272922.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesize the cDNA. First-stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned by the bynthesis primer was then restricted by digestion with XhOi, all XhOI sites in the CDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRI Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated vector (pBluescript II SX(+) that has been digested with ECORI and XhOI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Gen-c1027"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI, This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-4619"
/tissue_type="cotyledons of 3- and 7-day-old Williams seedlings"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:28463245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.4; DB 10 Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                              Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 496;
                                                                 MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                              Mus.
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ORIGIN

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COMMENT

FEATURES

High quality sequence stop: 425.

clone="IMAGE:6446341"

xref="taxon:10090"

strain="CD-1"

organism="Mus musculus" |mol\_type="mRNA" ocation/Qualifiers Seq primer: Primer name ambiguous

done by E.M. Eddy, Ph.D. (National Institute Institute of Environmental Health Sciences)

source

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

1 (bases 1 to 552)

Smith, T. P. L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF795982

State of the second 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="McCarrey Eddy spermatocytes"
/clone lib="McCarrey Eddy spermatocytes"
/stellibrary vector: pBluescript SK+
(Stratagene); Sitellibrary vector: pBluescript SK+
dT-primed [5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTTTT-3'] and
and 5'-CTCGTGCCG-3'. Size selection of +400bp material
and 5'-CTCGTGCCG-3'. Size selection of +400bp material
mass excised (from lambda-UniZAP-XR) and resulting
into pH10B. Library contains 98% recombinants.

Fifterences: J. Androl. 20:635-639 and Gene 25:263-269.
(Southwest Foundation for Blomedical Research, Dept. of
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH108 (phage-resistant)"
/clone_lib="McCarrey Eddy spermatocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="spermatocytes, pooled from multiple mice"
                                                                                                                                           phred v0.020425.c and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 512;
                                                                                            Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 21-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۰,
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                                                                                            with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                           ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       redex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Clone distribution: AGENAE Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.03
Sequence cleaned of vector, adaptator and repetitions. Contact us
sequence cleaned of vector, adaptator and repetitions of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 556)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library
Contact: Tosser-Klopp G
Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 GÁGGÁTGAÁGATGAÁGAGGÁGGÁCGÁGGÁGGÁCGÁGGATGAÁ 108
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Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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/mol_type="mRNA"
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/clone="scac0031i.e.12"
/clone="scac0031i.e.12"
/clone=lb="%us Scrofa library (scac)"
/clone=lib="%us Scrofa library (scac)"
/note="wector: pT713D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, nate of the process of the proce
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/mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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/db_xref="taxon:9823"
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Pred. No. 2.1e+02;
0; Mismatches 6
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COMMENT

Single pass sequencing. Bases called trimmed with the aid of the trim\_alt cross match v0.990329.

Plate: TMW8018 row: D column: 17

Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with

Contact: Smith TPL USDA, ARS, US Meat Animal PO Box 166, Clay Center, 1

ΝE

Research Center NE 68933-0166, USA

JOURNAL TITLE AUTHORS SOURCE ORGANISM

Sus scrofa (pig) Sus scrofa CF795982.1

GI:37800555

KEYWORDS

REFERENCE

RESULT 21 CF795982/c

DEFINITION

ACCESSION

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125

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Query Match Best Local S Matches

39,

Similarity 86.7 39; Conservative

69.4%;

0;

Score 35.4; DB 14; Pred. No. 2.1e+02; 0; Mismatches 6;

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RESULT 23
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Best Local Similarity
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Best Local S
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AI451753 586 bp mRNA linear mb16f09.y1 Soares mouse p3NMF19.5 Mus musculus cDNA IMAGE:329609 5' similar to TR:Q12804 Q12804 RECEPIN.
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BX676418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue CDNA Library
Unpublished (2003)
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 571)
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33 (0) 5.61.28.53.08
1: tosser@toulouse.inra.fr
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/mol_type="mRNA"
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/clone="scac00311.e.12"
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/clone lib="Sus Scrofa library (scac)"
/clone lib="Sus Scrofa library tissues: adipose tissue, hote="Vector: pT773D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"
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86.7%;
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Pred. No. 2.1e+02;
0; Mismatches 6;
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Pred. No. 2.1e+02;
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                    clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                      EST 15-MAR-2000
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AUTHORS
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Best Local
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                                                                                                                                                                                                                      227
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1 (bases 1 to 586)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                 CF367914 608
852497 MARC 3PIG Sus scrofa (
CF367914
                                                                                                                                                                                                                                                                                      39;
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AI451753.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                 Sus scrofa (pig)
Sus scrofa
                                                                  CF367914.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40RP from Gibco High quality sequence stop: 'POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:211009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:329609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                   GI:34172915
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                                                                                                                                                                                                                                                                                                    69.4%;
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                                                                                                                                                                                                                                                                                    Score 35.4; DB 9;
Pred. No. 2.1e+02;
0; Mismatches 6
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                                                                                                                  cDNA 3',
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   Euteleostomi;
Sus.
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; Murinae; Mus
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167 GAĞGAGGAĞATGAĞGAĞĞAĞĞAAĞAĞĞAAĞAĞAĞAĞAĞTĞAA 123
                                                                                                                                                                      Plate: TMW8012 row: I column: 1 Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                  Cross_match v0.990329.
Plate: TMW8012 row: I
                                                                                                                                                                                                                           Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                          Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. Porcine EST collection using a normalized library constructed from embryos representing early developmental stages (2003) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF792336
CF792336.1 GI:37796897
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885253 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
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Seq primer: TAGAAGGCACAGTCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross match v0.990329.
Plate: SRG8023 row: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
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Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,
Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.
A second set of porcine ESTs from a pooled-tissue normalized
                                                                                                                                                                                                                                                                                      smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                   /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tisue_type="pooled"
/lab_host="phil08"
/clone_lib="MARC_3PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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Pred. No. 2.1e.
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AUTHORS
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BY706040/c
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                                                                                                                                                                                                                                                                                                             Nikaido, I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saituk, H., Yamanaka, I., Schorbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Batalov, S., Beisel, K.W., Blake, J.A., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Matchionni, L., McKenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sultana, R., Takenaka, Y., Teded, D.J., Rend, J.D., Ranachandran, S., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Sultana, R., Yang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Sakai, K., Kawai, J., Alzawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Kawai, J., Alzawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Sohinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation ME. 2354683
     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., /
Fukuda,S., Hashizume,W., Hayashida,
                                                                                                        1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                        Nature 420,
22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 GAGGAAGATGAGGAGGAGGAAGAGGAAGAAGAAGAGAGTGAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 677)
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BY706040 RIKEN full-length enriched,
CDNA clone 1700012D21 5', mRNA seque
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/lab host="DH108"
/lab host="DH108"
/clome lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not!
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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Pred. No. 2.2e+02;
"" ematches 6;
imura, T., Arakawa, T., Carninci
Hayashida, K., Hirozane, T., Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA linear EST 16-DEC-2002
d, adult male testis Mus musculus
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FEATURES

RIKEN Genomic

230-0045, Japan

nci, P., Hori, F.,

source

JOURNAL COMMENT

TITLE AUTHORS SOURCE

KEYWORDS VERSION

DEFINITION ACCESSION RESULT 26 CF792336/c

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Query Match Best Local &

Local

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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                             BONRX59TR BO 1.6 2 KB genomic survey sequend BZ504700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome CBS. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                      BZ504700.1 GI:27024259 GSS.
                                                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                                         Brassica oleracea
                                                               Brassica oleracea
                                                                                                                                                                                             BZ504700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/db_xref="taxon:10090"
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/dev_stage="adult"
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                      Tracheophyta;
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishih,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Haradda,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
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Mus musculus adult male testis cDNA, RIKEN full-length enrich
library, clone:1700012D21 product:similar to CBF1 INTERACTING
COREPRESSOR CIR [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Other GSSs: BONRX59TF
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1 (bases 1 to 823)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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HTC; CAP trapper.
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Class: sheared ends.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole genome shotgun sequencing of Brassica oleracea
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/strain="TO1000DH3"
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/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
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S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramota, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M., Tagamia, T., Yasunishi, A., Yoshida, K., Direct Submission, M., and Hayashizaki, Y., Oshida, K., Direct Submission
1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
                                            39,
                                                                                                                                                                                                                                                                                                                                                                              was cleaved with XhoI and SstI. end: SstI. Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res.
20530913
11076861
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                                        Conservative
                                                                                                        /note="similar to CBF1 INTERACTING COREPRESSOR sapiens] (SPTR|095367, evidence: FASTY, 77.6%IP 96.4%length, match=1347)"
                                                                                                                                                                     /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                          /db_xref="FANTOM_DB:1700012D21"
/db_xref="MGI:1897524"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                  /clone="1700012D21"
                                                                                                                                                                                                                       gex="male"
                                                                                                                                                                                                                                                                                          mol_type="mRNA"
|strain="C57BL/6J"
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Tejima, Y., Toya, T., Yanamura, T., Yasunishi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Sohida, K., Direct Submission

Al Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama, Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (Dases 1 to 1595)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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AK008242

Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010015A19 product:similar to CBF1

INTERACTING COREPRESSOR CIR [Homo sapiens], full insert sequence.
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Sciurognathi; Muridae; Murinae; Mus.
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Search completed: February 29, 2004, 21:48:25 Job time : 2171 secs
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/db_xref="PANTOM DB:2010015A19"
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sapiens] (SPTR|095367, evidence: FASTY, 77.6%ID,
96.4%length, match=1347)"
                                                                                                                                                                                                     tiBsue type="small intestine"
/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/sex="male"
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; Patent No. 6500938
; GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHMAY GENE EXPRESSION

OUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
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Sequence 40, Appl
Sequence 40, Appl
Sequence 18762, A
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Strong, Theresa
APPLICANT: Conry, Robert M.

APPLICANT: LoBuglio, Albert F.

ITITE OF INVENTION: Melanoma Antigens and Methods of Use
FILE REFERENCE: D6253
CURRENT FILING DATE: 2000-10-18
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/160,042
PRIOR APPLICATION NUMBER: US 60/160,042
INUMBER OF SEQ ID NOS: 12
ILENTING DATE: 1999-10-18
SEQ ID NO 12
ILENTING OF SEQ ID NOS: 12
                                                밁
                                                                                     S
                                                                                                                                                                                             LENGTH: 593
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 3' end of clone 5.31 encoding a melanoma
US-09-691-538A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IENGTH: 2072 base pairs
TYPE: nucleic acid
STRANUBDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9178197
US-09-016-434-1181
                                                                                                                              Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-691-538A-12

; Sequence 12, Application US/09691538A

; Patent No. 6677444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.,
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKST NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1181:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                              Similarity
                    GĀGGĀGGĀGGAĀGATGĀGGĀGGĀCGĀGGĀGGĀĀGĀĞĀGĀGĀĞTGĀĀCČTCĀĞ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%;
91.7%;
                                                                                                                                        71.8%;
82.4%;
                                                                                                                Score 36.6; DB
Pred. No. 0.033;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                     4:
                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application:
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-9488
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                tent No.
                                                                                                                       APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: December 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/114,951
FILING DATE: August 31, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David S. Strayer and Avinash Chander
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Targeting Cells and Modulating Pulmonary Surfactant Secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 210 Lake CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single stranded
                                                                                            Boston
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                                                                         Massachusetts
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                                                                                                               60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Jane Massey Licata, Esq. 210 Lake Drive East, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.6%; Score 35; DB 88.4%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/176,218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-UULY-1993
APPLICATION NUMBER: US 07/643,982
APPLICATION HOWBER: US 07/643,982
APPLICATION TOWNER: US 07/643,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
     REFERENCE/DOCKET NUMBER: JD
                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                     NAME: Myers, Louis (PLM) REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICANT: White, Morris F.
PLICANT: Rothenberg, Paul Louis
TLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 GGAGGAGGCAGGAGGAGGAGGAGGAGGAGGAGGAGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCC
                                                                                                                                                                                                                                                                                                                                                           Boston
: Massachusetts
TRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                   02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application PC/TUS9609319
                                                                                                                                                                                                                                                                                                                                                                                                                           60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5125 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kahn, C. Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
589..4053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/094,948A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4:
                     JDP-013DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34.2; DB 1;
Pred. No. 0.19;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JDP-013DV
                                                                                                                                                                                                                                                   Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5125;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

4.

MOLECULE TYPE: CDNA

STRANDEDNESS: TOPOLOGY: lir

밁

GGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCC 49

99

0

PCT-US96-09319-4

NAME/KEY:

CDS 589..4053

Matches

Query Match Best Local /

Local Similarity

67.1%; 83.0%;

Score 34.2; DB 5; Pred. No. 0.19; 0; Mismatches 8;

.Length 5125; Indels

0,

Gaps

0,

Conservative

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US-09-621-976-18769; Sequence 18769, Ag; Patent No. 6639063
                                                                                                 RESULT 7
                                                                                                                                                В
                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
FEARLIER APPLICATION NUMBER: US 60/088,801
FEARLIER APPLICATION NUMBER: US 60/088,801
FEARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                      US-09-328-111-333
                            GENERAL INFORMATION:
                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(650)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                       Query Match
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     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 333
LENGTH: 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Steinmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carroll III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPPLICANT: Burgess, Christopher C.
                                                                                                                                                                                                                        Local
                                                                                                                                             245
                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333,
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Dumas Milne Edwards, J.B. Jobert, S.
                                                                                                                          ĠĀĠĠĀĠĠĀĠĀĀĠĀĀĠĀĀĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠGĀĀĠĀĀĀĀĀĊĀĊ 293
                                                                                                                                                                                                       Conservative
                                                      Application US/09621976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson O
                                                                                                                                                                                                                   79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kathleen E.
                                                                                                                                                                                           Score 33; DB 3;
Pred. No. 0.34;
0; Mismatches
                                                                                                                                                                                                  0,
                                                                                                                                                                                                                      DB 3; Length 650;
                                                                                                                                                                                           10; Indels
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CURRENT APPLICATION NUMBER: US/09/894,998A
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 34
LENGTH: 661
TYPE: DNA
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-894-998A-34
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; Sequence 34, Application US/09894998A
; Patent No. 6537555
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                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                  APPLICANT:
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Best Local S
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LENGTH: 404
TYPE: DNA
                                                PPLICANT
                                                                             PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: 210121.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 89.7
                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                           1085, Application US/09620312D
>. 6569662
                                                                                                                                                                                                                                                                                                   42 GAGGAGGAGGGAAGGAGGAGGAGGAGGCGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 GAGGAAGAAGGTCGGGAGGAAGAGGAGGAAGAAGAATGTGA 391
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Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGAGTGTGA 44
                                                                                   Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-bong
Zhao, Qing A.
Wehrman, Tom
                                          Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Ma, Yunqing
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 64.3%;
Similarity 84.1%;
37; Conservative
                             Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                            63.9%;
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Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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0,

Wang, Zhiwei John Tillinghaet

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APPLICANT: Drmanac, Radoje T.

ITITLE OF INVENTION: No. 65696221 Nucleic Acids and

ITITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER: 0F SEQ ID NOS: 1105

SOFTWARE: pt-Lgenes Version 1.0

SEQ ID NO 1085

LENGTH: 2817
                                                                                                         RESULT 11
US-09-702-705-1668
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US-09-620-312D-1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                        Sequence 1668, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local
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APPLICANT: Gure, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, LIOYd J.
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14561
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                               209 AGGGTGAGGAGGAAGAGGAGGAAGAGGAAGAAGAGGATGACC
                                                                                                                                                                                                                                                                                    37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                     GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA
Wang, Tongtong
Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                  63.1%;
ilarity 82.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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US-09-614-124B-1668

Sequence 1668, Application US/09614124B Patent No. 6630574 GENERAL INFORMATION:

APPLICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S.

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SOFTWARE: FastSEQ for Wi
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1668
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RESULT 13
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; ORGANISM: Homo sapiens
US-09-736-457-1668
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                                                                                                                                                                                                                          SOFTWARE: FAB
SEQ ID NO 1668
LENGTH: 636
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                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                Matches
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT FILING DATE: 2000-12-13
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 76.5%;
hes 39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG
                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCCAG 51
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Retter, Marc
Mannion, Jane
                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
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Fanger, Gary
Vedvick, Tom
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Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Bangur, Chaitanya
Lodes, Michael A.
                                                                                                              Conservative
                                                                                                                              62.48;
                                                                                                       ; Score 31.8; DB; Pred. No. 0.74; 0; Mismatches
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                                                                                                                12;
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Lodes, Michael A.

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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Reteer, Marc
APPLICANT: Reteer, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 21011.478C9
CURRENT APPLICANTON UNMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
SOFTWARE: FASCEGQ ID NOS: 1668
SOFTWARE: FASCEGQ for Windows Version 3.0
LENGTH: 636
TYPE: DNA
GRGANISM: Homo sapiens
US-09-614-124B-1668
                                                                                                                                                                                                                                    US-09-345-882-21
                                                                                                                                                                                                                                                                       RESULT 15
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; ORGANISM: Homo sapiens
US-09-671-325-1668
                                                                                                           Sequence 21, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
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APPLICANT: Bouguelexet, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FASCSEQ for Windows Version 3.0
LENGTH A 226

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Best Local
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                                                                                                                                                                                                                                                                                                             586 GÁGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGGAAGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 62.4%;
Similarity 76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAAGAGTGTGAAÇCCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 76.5
39; Conservative
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Lodes, Michael A
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Fan, Liqun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 0.74;
0; Mismatches 12; Indels
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Pred. No. 0.74;
0; Mismatches 12;
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US-08-574-959A-8
                                         Query Match
Best Local Similarity 85...
34; Conservative
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IENGTH: 258

ITYPE: DNA

ORGANISM: Homo sapiens
US-09-345-882-21
                                                                                                                                                                                                                                                                                                             COMPUTER REALIGHER FORM:

MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNBY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-574-959A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8,
Patent No.
                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                             MOLECULE TYPE: C
FEATURE:
NAME/KEY: CDS
LOCATION: 439.
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                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR ETLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES, TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8, Application US/08574959A
5. 5962224
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Similarity 89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 State Street, Suite 510
                                                                                                                                             439..3157
                                                                                                                                                                                                            linear
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                                                                         62.0%;
89.5%;
                                                  Score 31.6; DI
Pred. No. 0.96
0; Mismatches
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                                                                              DB 2; Length 3211;
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2590 GAGGAAGAAGAAGAGAGGAGGATGAGGAGGAGGAAGA 2627

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RESULT 18
US-08-574-959A-6
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US-09-357-014-8
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PACENT NO. 6221645

GENERAL INFORMATION:

APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi

APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi

TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USES THEREFOR
                                                                                                                                                                                                          Sequence 6, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
GENERAL INFORMATION:

APPLICANT: Jackycon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

TITLE OF INVENTION: AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-U1-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
PRIOR APPLICATION UMBER: 08/574,959
PRIOR DATE: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              2590 GAGGAAGAAGAAGAGGAGGATGAGGAGGAGGAAGA 2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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LOCATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.6; DB Pred. No. 0.96;
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Matches
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RESULT 19
US-09-357-014-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: 1
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          SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Uu1-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
FILING DATE: <UNKnown>
APPLICATION THEORNATION:
NAME: MANDER: AUKNOWN>
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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mes 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/574,959A FILING DATE: 19-DEC-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, AND USES THEREFOR
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3280 GAGGAAGAAGAAGAAGAGGAGGATGAGGAGGAGGAAGA 3317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02109-1875
                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                 ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.0%; Score 31.6; DB ilarity 89.5%; Pred. No. 0.98; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : (617)227-7400
(617)227-5941
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439..3847
                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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INFORMATION

WATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

TELEPHONE: (617)227-7400 TELEFAX: (617)227-5941

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                                                                                                                  US-09-620-312D-480
                                                Query Match
Best Local Similarity 89.5
                                                                                                                                                           NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 480
LENGTH: 4226
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-620-312D-480
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                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-357-014-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equenc.
Patent NO. 6565000-
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
                                                                                                                             NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zinwei
APPLICANT: Wang, Zinwei
APPLICANT: John Tillinghast
APPLICANT: Drmannac, Radoje T.
TITLE OF INVENTION: No. 6559662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
658 GATGAAGAAGCAGAAGAAGAAGAAGAAGAAGAAGA 695
                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3280 GÁGGAAGAÁGAAGAÁGÁGGÁGGÁTGÁGGAGGÁÁGÁ 3317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang, J.C.
Ren, Feiyan
Chen, Rui-hong
Canao, Qing A.
Crman, Tom
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34; Conserv
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6569662
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                                                                                                                                                                                                                                                                                                                                                                                                                             Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi, Jie
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STRANDEDNESS: single
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                                                                    62.0%;
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89.5%;
                                                   ; Score 31.6; DB ; pred. No. 0.99; 0; Mismatches
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Pred. No. 0.98;
0; Mismatches 4;
                                                                        DB 4; Length 4226;
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RESULT 21
US-09-345-882-4
    FEATURE:
NAME/KRY: allele
LOCATION: 1921..1967
OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID62
                                                                         NAME/KEY: allele
LOCATION: 1921..1967
OTHER INFORMATION: po
                                                                                                                              NAME/KEY: allele
LOCATION: 1315..1338
OTHER INFORMATION: po
                                                                                                                                                           FEATURE:
NAME/KEY: allele
LOCATION: 1315..1338
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: allele
LOCATION: 1107..1125
OTHER INFORMATION: po
NAME/KEY: allele
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SEQ ID NO 4
LENGTH: 6002
                                                                                                                        FEATURE
                                                                                                                                                                                                                             OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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NAME/KEY: allele
LOCATION: 1338
OTHER INFORMATION: 5
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Patent No. 63777.
Patent INFORMATION:
                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 1107..1125
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Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 5-148-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3346
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 3329
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1944
OTHER INFORMATION:
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
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LOCATION: 1319
OTHER INFORMATION:
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LOCATION: 3329
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NAME/KEY: allele
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                                                                  polymorphic fragment 5-136-174 SEQ ID41
                                                                                                                         polymorphic fragment
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NAME/KEY: allele
LOCATION: 3323..3369
OTHER INFORMATION: polymorphic
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LOCATION: 1296..1338
OTHER INFORMATION: polymorphic
             NAME/KEY: misc_feature
LOCATION: 844..1303
                                              LOCATION: 818. 1306
OTHER INFORMATION: complement
                                                                                                                                                                                                       LOCATION: 209.756
OTHER INFORMATION: homology
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LOCATION: 3323..3369
OTHER INFORMATION: polymorphic
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LOCATION: 3306..335
OTHER INFORMATION:
                                                               NAME/KEY: misc_feature
                                                                                                    OTHER INFORMATION: complement
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LOCATION: 391..815
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OTHER INFORMATION: potential
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LOCATION: 453..898
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LOCATION: 442..444
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OTHER INFORMATION: po
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OCATION: 5896..5901
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ACATION: 4878..4883
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OTHER INFORMATION: ATG
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OTHER INFORMATION: polymorphic
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INFORMATION: complement homology
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5981..5986
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5116..5121
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 emb1:AA262427
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                                                                               GENERAL INFORMATION:
APPLICANT: BOUGUELETCI, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REFERENCE: GENSET.031A
                                                                                                                                                  Sequence 1, Application US/09345882 Patent No. 6399373
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
CURRENT APPLICATION NUMBER: US/09/345,882 CURRENT FILING DATE: 1999-06-30 PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10
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LOCATION: 1351..1702
OTHER INFORMATION: complement homology
FEATURE:
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LOCATION: 5580..6002
OTHER INFORMATION: complement
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OTHER INFORMATION: homol
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LOCATION: 3883..4221
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LOCATION: 2181..2281
OTHER INFORMATION: home
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LOCATION: 4516..5016
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LOCATION: 2480..2842
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OTHER INFORMATION: homology
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LOCATION: 2253..2482
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LOCATION: 1866..2109
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Pred. No. 1;
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NUMBER OF SEQ ID NOS: 140 SOFTWARE: Patent.pm EQ ID NO 1

ENGTH: 162450

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FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION:
                 NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION:
                                                 LOCATION: 134362
OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
                                             FEATURE:
                                                            NAME/KEY: allele
LOCATION: 134362
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LOCATION: 108149
OTHER INFORMATION: !
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NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5
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OTHER INFORMATION:
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LOCATION: 108471
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LOCATION: 106940
OTHER INFORMATION:
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LOCATION: 108308
OTHER INFORMATION:
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LOCATION: 99098
OTHER INFORMATION: 5
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LOCATION: 93714
OTHER INFORMATION: 5
FEATURE:
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NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION:
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THER INFORMATION:
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THER INFORMATION:
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LOCATION: 97122
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OTHER INFORMATION:
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LOCATION: 90842
OTHER INFORMATION:
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LOCATION: 88073
OTHER INFORMATION: 5-127-261
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LOCATION: 72794
OTHER INFORMATION:
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               5-140-361
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FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polyn
NAME/KEY: allele
LOCATION: 99094..99140
                            NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic
FEATURE:
                                                                              NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: pol
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REATURE:
NAME/KEY: allele
'CaTION: 93690..93736
'CaTION: Polymorphic fr
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LOCATION: 97130..97177
OTHER INFORMATION: pol-
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NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic
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LOCATION: 93690..93
OTHER INFORMATION:
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OTHER INFORMATION: complement polymorphic
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OTHER INFORMATION:
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LOCATION: 88050..86
OTHER INFORMATION:
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LOCATION: 72771..72817
THEOREMATION: polymorphic fragment 5-124-273
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LOCATION: 90819..
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OTHER INFORMATION: polymorphic fragment
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LOCATION: 72771..72817
OTHER INFORMATION: pol
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LOCATION: 160031
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 150329
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LOCATION: 146345
OTHER INFORMATION:
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OTHER INFORMATION:
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DN: polymorphic fragment 5-127-261
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                          fragment 5-130-257 SEQ ID55
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OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35

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CURRENT APPLICATION NUMBER: US/09/817,310
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 09/230,247
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2556
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-817-310-1
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Query Match
Best Local Similarity
Matches 38; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                     APPLICANT: Stewart, Mary
APPLICANT: Kozma, Sarah
APPLICANT: Thomas, George
TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
FILE REFERENCE: 4-20971/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 108127
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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OTHER INFORMATION:
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LOCATION: 103783..103828
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OTHER INFORMATION: polymorphic
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LOCATION: 106918
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LOCATION: 106918
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LOCATION: 103783.
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89.5%;
                  61.6%;
 Score 31.4; DE
Pred. No. 1.1;
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Pred. No. 1.4;
0; Mismatches
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US-09-702-705-309/c
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US-09-736-457-309/c
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                                           SOFTWARE: Fa
SEQ ID NO 309
LENGTH: 129
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LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                      Sequence 309, Application US/09736457 Patent No. 6509448
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Best Local
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                                                                                     CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 183
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
                                                                                                                                  APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
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APPLICANT: Lodes, Michael
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (1)...(129)
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6504010
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Carter, Darrick
Retter, Marc
Mannion, Jane
                                                                         FastSEQ for Windows Version
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Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Lodes, Michael
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Bangur, Chaitanya
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Pred. No. 0.94;
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; LOCATION: (1)...(129)
; OTHER INFORMATION: n = A,T,C or
US-09-736-457-309
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C12
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SEQ ID NO 309
LENGTH: 129
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APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marrick
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
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Best Local Similarity
Matches 36; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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LOCATION: (1)...(129)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Wang, Tongtong
Tongur, Chaitanya &
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Lodes, Michael
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Lodes, Michael A.
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Pred. No. 0.94;
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                                                                                                            Sequence 18731, Appl Patent No. 6639063 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 309
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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US-09-589-184-309/c
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                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(129)
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.47868
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(129)
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Wang, Chaitanya S
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Carter, Darrick
Retter, Marc
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Lodes, Michael
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Pred. No. 0.94;
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Sequence 18711, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET, 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 18711

LENGTH: 427

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

LOCATION: 72,215,229

OTHER INFORMATION: n=a, g, c or t
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; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18731
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Search completed: February 29, 2004, 22:26:08 Job time: 65.5 secs
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US-09-621-976-18711
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                                                                                       343 GAGGAAGAAGGTGGGGAGGAAGAAGAAGAAGAAGAAGGTGA 386
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Post-processing: Minimum Match 0%
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

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5: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US108_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US108_NEW PUB.seq:*
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Match Length
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       2353733 seqs, 1803733377 residues
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14 US-10-001-073-2

9 US-09-825-923-1

14 US-10-077-870-1

14 US-10-077-870-1

14 US-10-077-870-3

4 US-10-001-073-1

5 US-10-001-073-1

4 US-10-225-567A-41

4 US-10-128-714-6204

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1 US-10-128-714-590-139707

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Sequence 14712, Ap
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Sequence 2316, Ap
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Sequence 10070, Appl
Sequence 27424, Appl
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RESULT 1
US-10-001-073-2
i Sequence 2, Application US/10001073
i Publication No. US20030113725A1
i GENERAL INFORMATION:
i APPLICANT: Liggett, Stephen
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15 US-10-242-535A-18689
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15 US-10-242-535A-18689
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18 US-10-113-872-1668
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Sequence 329, App
Sequence 329, App
Sequence 1085, Ap
Sequence 1085, Ap
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Sequence 113941,
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Sequence 1657, Ap
Sequence 304, App
Sequence 51, Appli
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Sequence 1668, Ap
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Sequence 1907, App
Sequence 19074, App
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Sequence 750, App
Sequence 750, App
Sequence 760, App
Sequence 760, App
Sequence 776, App
Sequence 480, App
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Sequence 312, App
Sequence 9110, App
Sequence 111, App
Sequence 1309, App
Sequence 1309, App
Sequence 133743,
          RESULT 3
US-10-077-870-1
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US-09-825-923-1
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GENERAL INVORMATION:

APPLICANT: Hainonen, Paula
APPLICANT: Hainonen, Paula
APPLICANT: Karvonen, Matti
APPLICANT: Karvonen, Matti
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Marku
APPLICANT: Koulu, Marku
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Tuomainen, Ullamari
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Wysse'nen, Kristiina
APPLICANT: Walkonen, Jussi
APPLICANT: Kauhanen, Jussi
APPLICANT: Walkonen, Veli-Pekka
TITLE OF INVENTION: Protein, and uses thereof
TITLE OF INVENTION NUMBER: US/09/825,923
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
CRGANISM: Homo sapiens
FEAURE:
NAME/KEY: CDS
CURRENT INFORMATION: Alpha-2B-adrenoceptor protein
US-09-825-923-1
; Sequence 1, Application US/10077870
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Patent No. US20010016338A1
GENERAL INFORMATION
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TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION UNMERE: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
COCANICAL TABLES OF SERVICE OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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96.1%;
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Pred. No. 9.5e-06;
0; Mismatches 2
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APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a ri-
FILE REFERENCE: 0933-0183p
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 1
RESULT 5
US-09-825-923-3
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LENGTH: 6904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
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CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OLEK, APPLICANT: PIEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2424
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TYPE: DNA
                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 6084
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                 OTHER INFORMATION: n is a
                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: chemically treated genomic
                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                           5880
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                                                                                                                 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
                                                                                                                                                                       Similarity
                                                                         GAGGATGAAGTTGAAGAGGAGGAGGAGGAAGATTGTGAA 5924
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No. US20030143606A1
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95.6%;
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Pred. No. 9.5e
0; Mismatches
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Pred. No. 0.00064;
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APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: method for detecting a
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10077870 Publication No. US20030003470A1
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SEQ ID NO 3
Query Match 81.6%;
Best Local Similarity 91.7%;
Matches 44; Conservative
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Best Local (
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Valkonen, Vali-Pekka
APPLICANT: Valkonen, Vali-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                         LENGTH: 13
                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 3.1
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
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                                                                                         NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                       FEATURE:
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Salonen, Jukka T
Salonen, Tomi-Pekka
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Nyyss"nen, Kristiina
Salonen, Riitta
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91.7%;
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Score 41.6; DB 14;
Pred. No. 0.00075;
0; Mismatches 4;
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Pred. No. 0.00075;
0; Mismatches 4;
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; Sequence 41, Application US/10225567A; Publication No. US20030113798A1; GENERAL INFORMATION:
                                                                                 US-10-225-567A-41
                                                                                                      RESULT 9
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                                                                                                                                                                                                                                                                    ; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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US-10-305-720-1181
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION UNMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTMARE: PERL PROGram
SEQ ID NO 1181
LENGTH: 2072
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APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                    Query Match
Best Local (
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Best Local S
Matches 44
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Publication No. US20040010136A1
GENERAL INFORMATION;
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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Publication No. US20030113725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                    Similarity
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Pred. No. 0.00074;
0; Mismatches 4;
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Pred. No. 0.00075;
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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEO ID NOS: 8603
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8603

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6204

LENGTH: 2367

TYPE: DNA

ORGANISM: Aspergillus fumigatus
US-10-128-714-6204
RESULT 11
US-10-128-714-7204
US-10-128-714-7204
; Sequence 7204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
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Best Local &
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LENGTH: 3274
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                          70.6%;
11 Similarity 88.6%;
39; Conservative
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Pred. No. 0.038;
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Pred. No. 0.00074;
0; Mismatches 4;
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; ORGANISM: Aspergillus fumigatus US-10-128-714-204
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                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PPLICATION NUMBER: US 60/287,066
PRIOR PPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PRILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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SEQ ID NO 7204
LENGTH: 2367
TYPE: DNA
  Query Match
                                                                                                                                                    SEQ ID NO 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REPERENCE: 10182-018-999
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PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/316,362 PRIOR FILING DATE: 2001-08-31
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CURRENT FILING DATE: 2002-04-23
                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                  TYPE: DNA
                                                                                                                          LENGTH: 4238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-06-05
APPLICATION NUMBER: US 60/303,899
FILING DATE: 2001-07-09
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                                                                                                                                                                           PatentIn
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                                                                                                                                                                              version
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                                                                                                                                                                                                                             2001-08-31
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  70.6%; Score 36;
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Pred. No. 0.038;
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  BB
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  14;
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Length 4238;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for INTERITY APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 139707
LENGTH: 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-128-714-5204
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; OTHER INFORMATION: Clone ID: US-10-424-599-139707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 5204
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                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 139707, Application US/10424599 Publication No. US20040031072A1
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and TITLE OF INVENTION: Methods of Use
FILE REPERROCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-3
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8603
                                                                     TYPE: DNA
ORGANISM: Glycine max
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                                                 FEATURE:
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88.6%;
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Pred. No. 0.03
0; Mismatches
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                      PAT_MRT3847_97163C.1
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ROVALL DAVID ROVALL DAVID K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53223)B
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 94653
LENCTH: 1554
TYPE: Particular Security Securit
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Best Local Similarity
Matches 41; Conserv
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US-09-864-408A-3111
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APPLICANT: Leach, Michard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANTON: US20040009474Alel Human Polynucleotides and Polypeptides Encountry
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2006-8906
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3111
SEQ ID NO 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 311, Application US/09864408A Publication No. US20040009474A1
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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Similarity 84.8%;
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[milarity 82.0%;
Conservative (
              85
                                                                                                                                                                                                                                                                                  1 Similarity
38; Conserv
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                                                                                                               GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGA 44
                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 0.051;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                Score 34.4; DB 11;
Pred. No. 0.12;
0; Mismatches 6;
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RESULT 17

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APPLICANI: CASTLE, Arthur
APPLICANI: CASTLE, Arthur
APPLICANI: CLASHOFF, Michael
APPLICANI: ELABHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
TILE REFERENCE: 44921-5090US
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_013040 US-10-191-803-61
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                                                                                                                                                                                                                                                              APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
APPLICANTON: OVARY SPECIFIC GENES AND PROTEINS
TILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION UNMBER: US/09/844,864
CURRENT FILING DATE: 201-04-27
CURRENT FILING DATE: 201-04-27
PRIOR APPLICATION UNMBER: P07/US99/25209
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
NUMBER: OF SEQ ID NOS: 25
PRIOR FILING DATE: 1999-10-38
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US-09-844-864-12
| Sequence 12, Application US/09844864
| Sequence 12, Application US/09844864
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SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 61
                                                                                                                                                  ORGANISM: Mus musculus
US-09-844-864-12
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Best Local &
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                                                                      Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
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                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                            ENGTH: 182
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GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
                               1 GAGGATGAAGACTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
                                                                                                Similarity
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Pred. No. 0.12;
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Pred. No. 0.19;
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US-10-424-599-108927
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                                                                                                           RESULT 21
US-10-369-493-27799
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Sequence 27799, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas
APPLICANT: Kovalic David
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 108927
LENGTH: 2526
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APPLICANT: WL, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: FCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_69375C.1
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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nes 38; Conservative
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les 38; Conserv
                                                                                                                                                                                               528 GAAGATGACGAGGAAGAGGAGGAAGAGGAAGAGGATGAA 572
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Zhou Yihua
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                                                                                                                                                                                                                                                                              Mismatches
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; Sequence 23094, Application US/09864761
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                                                                                                                                                                                                                                   RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
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SEQ ID NO 27799
LENGTH: 3401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 145
                                                                                                                                           Patent No. US20020048763A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 145, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in |
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 117
NUMBER OF SEQ ID NOS: 177
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: "Hanzel, David K.
APPLICANT: "Hanzel, David K.
APPLICANT: Chen, Wensheng
TITIE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
PILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: RNA1 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                1427 GAAGATGATGAGGAGGAGGAGGAGGAGGAAGAGGAAGAGCCCTCCG 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3129 GAGGATGACGAAGAAGAGGAAGAGGAAGAAGAAGAAGTAGGGA 3173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                       1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldman, Barry S. Chen, Xianfeng NVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10205194
o. US20030134301A1
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                                                                                                                                                                                                                                                                                                                                                                            65.5%; Score 33.4; DB 78.4%; Pred. No. 0.24; cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.8; DB Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2981;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

ION NUMBER: US 60/180,312

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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELLCATION NUMBER: PCT/USO1/00665
PRIOR PELLOATION UNMBER: PCT/USO1/00668
PRIOR PELLCATION UNMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLOATION NUMBER: US 09/608,408
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLOATION NUMBER: US 09/608,408
PRIOR PELLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHENIUSE INFORMATION: MAP TO ACOU4687.1

OTHER INFORMATION: EXPRESSED IN FIRL LYDR, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN ADULT LITER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN ADULT LITER, SIGNAL = 2.6

OTHER INFORMATION: SWISSPROT HIT: P51450, EVALUE 8.70e-02

OTHER INFORMATION: SWISSPROT HIT: EVALUE 1.00e-36

OTHER INFORMATION: EST_HUMAN HIT: A1653251.1, EVALUE 2.00e-36

OTHER INFORMATION: EST_HUMAN HIT: A1653251.1, EVALUE 2.00e-36
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IOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
RESULT 24
US-09-918-995-27029
US-09-918-995-27029, Application US/09918995
Sequence 27029, Application US/030073623A1
Publication No. US20030073623A1
OR GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                       Conservative
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PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PLING DATE: US/09/235,076
PRIOR PLING DATE: US/09/235,076
PRIOR PLING DATE: 1999-01-20
VALUMBER OF SEQ ID NOS: 38054
NUMBER OF SEQ ID NOS: 38054
NUMBER OF SEG ID NOS: 38054
NUMBER 
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US-09-918-995-27029
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REPERENCE: 20411-756 FILE REPERENCE: 20411-756 FILE REPERENCE: 20411-756
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Best Local S
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CURRENT FILING DATE: 2001-07-30
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                                                                              PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03 4263.6
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELLING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456
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35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGA
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US20020048763A1
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VIG DATE: 2000-09-21
VIG DATE: 2000-09-30
VIG DATE: 2000-06-30
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Pred. No. 0.2
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PRIOR APPLICATION NUMBER: US 09/774,203

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OTHER INFORMATION: MAP TO ACO04687.1

OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.6
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                                                                                                                                          US-09-879-536-333
                                                                                                                                                                     RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43536
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CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR PELICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-02-28
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Best Local S
Matches 35
Sequence 333, Application US/09879536
PATENT NO. US20020144298A1
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: PatentIn version 3.2
SEQ ID NO 43536
LENGTH: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43536, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6378
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing
FILE REFERENCE: 4231/2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 492
                                                                                                                                                                                                                                         185
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                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
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                                                                                                                                                                                                                                         GAGGAGGAAGAAGAAGAAGAAGGAGGAGGAGGAGGAAGAAACAC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAGGAAGAGGAGGAGGAGGAGGAAGAG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAG 39
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                        64.7%;
                                                                                                                                                                                                                                                                                                                                Score 33; DB:
Pred. No. 0.32
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   0,
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Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                              DB 15;
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                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                              Length 390,
                                                                                                                                                                                                                                                                                                                                   Indels
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/879,536

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION UNMBER: US 60/088,801

PRIOR FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 333

LENGTH: 650

Type: Nos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens FEATURE:
; NAME/KEY: misc.feature; LOCATION: (1)...(650); OTHER INFORMATION: n = A,T,C.US-09-879-536-333
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60174, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                              Best 'Local
Matches
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 60174
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
FILE REFERENCE: 38-21 (53223) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                               LENGTH: 1634
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                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCC
                                                                                                                              39;
                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derti, Adnan
Ford, Donna M.
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Bushnell, Steven E.
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ilarity 79.6%;
Conservative
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79.6%;
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Pred. No. 0.32
0; Mismatches
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                                                                                                                          Score 33; DB 12; Length 1634; Pred. No. 0.32; O; Mismatches 10; Indels
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US-10-029-386-18468; Sequence 18468, Application US/10029386; Publication No. US20030194704A1